

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 17, 2005, 00:47:35 ; Search time 40 Seconds  
(without alignments)  
894.816 Million cell updates/sec

Title: US-10-716-489-2

Perfect score: 1951

Sequence: 1 MSTAAALITLVRSQGNVRRR.....KNSINFSPFSSGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	360	18.5	348	T50783	protein phosphatas
2	357	18.3	383	T48018	hypothetical prote
3	344.5	17.7	392	T84650	probable protein p
4	338	17.3	434	T04263	phosphoprotein pho
5	337.5	17.3	381	T09640	protein phosphatas
6	332.5	17.0	359	T52337	phosphoprotein pho
7	328	16.8	362	T84695	probable protein p
8	326	16.7	464	T896700	protein F12A21.5
9	325	16.7	281	T41854	phosphoprotein pho
10	322.5	16.5	239	T01361	probable protein p
11	322.5	16.5	816	T48123	hypothetical prote
12	322	16.5	511	T89752	protein phosphatas
13	321.5	16.5	347	T456058	phosphoprotein pho
14	320	16.4	355	T84643	probable protein p
15	319.5	16.4	389	T05095	hypothetical prote
16	319.5	16.4	390	T820392	phosphoprotein pho
17	319.5	16.4	397	TJ2524	phosphoprotein pho
18	318.5	16.3	423	T48121	hypothetical prote
19	318	16.3	238	T96811	hypothetical prote
20	311.5	16.0	361	T45778	protein phosphatas
21	310.5	15.9	383	T38772	protein phosphatas
22	307.5	15.8	382	T82423	phosphoprotein pho
23	307.5	15.8	390	T85672	phosphoprotein pho
24	307.5	15.8	393	T49016	phosphoprotein pho
25	307.5	15.8	396	T02483	probable protein p
26	306.5	15.7	382	T82422	phosphoprotein pho
27	306.5	15.7	382	T53823	magnesium dependen
28	306.5	15.7	382	T32399	phosphoprotein pho
29	306.5	15.7	414	T82462	protein phosphatas

protein phosphatas  
probable protein p  
protein F22G5.22  
protein phosphatas  
probable protein p  
phosphoprotein pho  
protein phosphatas  
T16E15.10 protein  
probable protein p  
probable protein p  
probable protein p  
phosphoprotein pho  
phosphoprotein pho  
hypothetical prote  
probable protein p  
protein T23F11.1

## ALIGNMENTS

### RESULT 1

T50783  
protein phosphatase 2C-like protein - Arabidopsis thaliana  
N;Alternate names: protein T30N20\_10  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004  
C;Accession: T50783  
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirksen, W.; Stiekema, W.; Bancroft, I.; Mew  
submitted to the Protein Sequence Database, July 2000  
A;Reference number: Z25240  
A;Accession: T50783  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-348 <BEV>  
A;Cross-references: UNIPROT:Q9LEW5; EMBL:AL365234  
A;Experimental source: cultivar Columbia; BAC clone T30N20  
C;Genetics:  
A;Map position: 5  
A;Introns: 27/2; 70/1; 103/1; 156/1; 185/1; 209/3; 234/3  
A;Note: T30N20\_10  
C;Superfamily: human phosphoprotein phosphatase 1A

Query Match 18.5%; Score 360; DB 2; Length 348;  
Best Local Similarity 35.4%; Pred. No. 1.3e-22;  
Matches 99; Conservative 56; Mismatches 89; Indels 36; Gaps 11;  
Qy 96 GCASQIGRKENEEDRP--FAQLTDEVL-YFAYVDHGGPAADFCPTHHEKICIMDLLPK 152  
Db 35 GYASSAGKRSMEDFFPETRIDGINGEIVGLFVFDHGGARAAEYVKRHL---FSNLITH 91  
Qy 153 EK--NLETLTLTFLAFLDID---KAFSSHARLSADATLLTSGTTATVALLRDGIELVVAS 205  
Db 92 PKFISDTQSAITDAYNHTDSELLKSENHR-----DAGSTASTAIL-VGRLVVAN 142  
Qy 206 VGDRAILCKGPKMLTIDHTPERKDEKRIKCGFVAVNSLQGFVNGRLAMTRSIG 265  
Db 143 VGDRAVISGGKAIASVRDHKPDQSDERIERIENAGGFVWM-----AGVLAVSRAFG 194  
Qy 266 DLDLTKTSGVIAEPETKRIKULHADDSS--FLVLTDTGTFMNVNSQIEICDFVNCQHDPEAA 323  
Db 195 DRLLK-QYVVADPEIQEKI---DDTLEFLILASDGLWDVFSNEAAVAMVKEVEDPEDSA 250  
Qy 324 HAVTEQAIQGTEDNSTAVVVPFGAWGKYKNSEINFSPSR 363  
Db 251 KKLVGGAIKRGSADNITCVVVVRFLEKKSASSSHISSSSK 290

### RESULT 2

T48018  
hypothetical protein T1J713.220 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004







Db	311	GSSDKVLEAVAS-ETVGSTAVVALVCCS-HIIVSNSCGDSRAVLFRGKEAMPLSVDPKPD	368
Qy	231	KDEKERIKKCGG-FVAMNSLQCPHVNGHRLMTRSIGDLDLKTSGVIAPETXRIKLHHAD	289
Db	369	EDEVARIENAGGKVIQMGQ---ARVFGVLAMSRSIGDRLYKPY-VIPEPVTFMP-RSRE	423
Qy	290	DSFLVLTYDGINFMVNSQEI CDFVNO-----CHDPN-----EAAHAVTE	328
Db	424	DECLILASDGLWDVNNNGVEICEIARRRILMWHKKNGAPPLAERGKGIOPACQAAADYLSM	483
Qy	329	QAIQYGTEDNSTAVVVPFGANGKYK	353
Db	484	LALQKSKDNISIIIVDLKAQRKPK	508

A:Molecule type: DNA  
A:Residues: 1-355 <STO>  
A:Cross-references: UNIPROT:O81716; GB:AE002093; NID:g4559345; PIDN:AAD23006.1; GSPDB:GNCN  
C:Genetics:  
A:Gene: At2g25070  
A:Map position: 2  
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 16.4%; Score 320; DB 2; Length 355;  
Best Local Similarity 30.8%; Pred. No. 3.1e-19;  
Matches 96; Conservative 44; Mismatches 104; Indels 68; Gaps 9;

Qy 96 GCASQIGKRKENED-RFDFAQLTDEVLYFAVYDGHGGPAAADFCHTHM-EKCTIMDLLPKE 153  
Db 25 GLSSMQGWRATMEDAAHAILDLDDKTSFFGVYDGHGGKVVAKFCAKYLHQOVISNEAYKT 84  
Qy 154 KNLFTLLTFLAFLD-----KAFSSSHARLS----- 178  
Db 85 GDVETSLRRATFRDMDMMQGGWRGLAVLGDMKMKFSGMIEGFIWSPRSGDTNNQPDWS 144  
Qy 179 -----ADATLLTSGTTATVALLRDGIELVVASVDGSRAILCRKGPMLKLTIDHTPERK 231  
Db 145 PLEDGPHSDFTPISGCTACVALIKDK-KLFVANAGDSRCVLSRKSOAYNLSKDKHPDLE 203  
Qy 232 DEKERIKKCGGFVAVNSLUGQPHVNGRLAWTRISGLDLTKTSG-----VIAEPETKRI 283  
Db 204 VEKERILKAGGFI-----HAGRINGSLLNLTALIGDMFEFKQNKFLPSEKQWVTADPDINTI 258  
Qy 284 KLHHADSFVLTTDGINFMVNSQBIQCPVNOCHDPNEAAHVAITEQAIQVGTB----- 336  
Db 259 DLCD-DDDFLVVACDGIWDCMSSQBELVDFIHEQLKSETKLSTVCEKVDRCCLAPDTATGE 317  
Qy 337 --DNSTAVVVPF 346  
Db 318 GCDNNYILVQF 329

RESULT 15  
T05095  
hypothetical protein F28M20.60 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T05095  
R:Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, F.  
submitted to the Protein Sequence Database, November 1998  
A:Reference number: 215398  
A:Accession: T05095  
A:Molecule type: DNA  
A:Residues: 1-389 <BEV>  
A:Cross-references: UNIPROT:O81773; EMBL:AL0311004  
A:Experimental source: cultivar Columbia; BAC clone F28M20  
C:Genetics:  
A:Map position: 4  
A:Introns: 95/1; 128/1; 181/1; 210/1; 274/3; 318/3  
A:Note: F28M20.60  
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 16.4%; Score 319.5; DB 2; Length 389;  
Best Local Similarity 30.8%; Pred. No. 3.9e-19;  
Matches 97; Conservative 45; Mismatches 92; Indels 81; Gaps 11;

Qy 96 GCASQIGKRKENED-----RFDFAQLTDEVLYFAVYDGHGGPAAADFCHTHMERKIMDLLP 151  
Db 60 GYASSPGKRSSMEDFYETRIDGVE-GEIVGLFGVFDGHGGARAAEYVKQNL---FSNLIR 115  
Qy 152 KEKNLETLTLLTFLAFLDIDKAFSSSHARLSADATLLTS-----GTTATVALLRDGIELVV 203  
Db 116 HPK-----FISDTTAAIADANQTDSEFLKSQNSQNRDAGSTASTAIL-VGDRLLV 165  
Qy 204 ASVGDSRAILCRKGPMLKLTIDHTPERKDEKERIKKCGGFVAVNSLUGQPHVNGRLAWTR 263  
Db 166 ANVGDSRAVICRGNAITAVSRDHPQSDERQKIEDAGGFVWV--AGTRVGVGVLAVSRA 223

Qy	264	IGDLDKTSGVIAEPE-----TKRIKLHH-----	287
Db	224	FGDLLEK-QYVADPEIQVLTFCQNLLEYIKNATLLTIEHNLHWISIVSYLNGTLQNFL	282
Qy	288	-----ADDS--FLVLTDDGINFMVNSOEICDFVNOCHDPNEAAHATEQAI	331
Db	283	RSLISINGKFOEEKVDSLEFLILASDGLWDVVSNEEAVGMKAIEDPEEGAKRLMMEAY	342
Qy	332	QYGTEDNSTAVVVPF	346
Db	343	QSGADNITCVCVVRP	357

Search completed: June 17, 2005, 00:57:51  
Job time : 43 secs

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## OM protein - protein search, using sw model

Run on: June 17, 2005, 00:39:24 ; Search time 171 Seconds  
(without alignments)  
1113.997 Million cell updates/sec

Title: US-10-716-489-2

Perfect score: 1951

Sequence: 1 MSTAALITLVRSQGNVRRR.....KNSEINFSPRSFSSGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1951	100.0	372	2	Q8N3J5
2	1950	99.9	372	2	Q6EN45
3	1945	99.7	372	2	Q8IUT7
4	1777	91.1	372	2	Q8BXN7
5	1399.5	71.7	372	2	Q6ING9
6	951.5	48.8	233	2	Q8IXG7
7	950	48.7	182	2	Q8ND70
8	369	18.9	348	2	Q67UX7
9	369	18.9	354	2	Q8LAY8
10	360	18.5	348	2	Q8LEW5
11	358	18.3	290	2	Q6IV73
12	357	18.3	383	2	Q9MIP8
13	354.5	18.2	352	2	Q653S3
14	354.5	18.2	362	2	Q653S4
15	354.5	18.2	423	1	P2C2 ARATH
16	352	18.0	282	2	Q7XR06
17	350.5	18.0	303	2	Q81OH0
18	350.5	18.0	360	2	Q8BHN0
19	350.5	18.0	360	2	Q8C021
20	348	17.8	319	2	Q8S820
21	348	17.8	491	2	Q6L5C4
22	346.5	17.8	388	2	Q8H610
23	344.5	17.7	392	2	Q9SLA1
24	344	17.6	311	2	Q8RXV3
25	344	17.6	420	2	Q8VZD9
26	342	17.5	394	2	Q84QD6
27	342	17.5	420	2	Q94AT1
28	340.5	17.5	380	2	Q9FYN7
29	338.5	17.4	276	2	Q6FWM3
30	338	17.3	434	1	P2C1 ARATH
31	337.5	17.3	381	2	O24078

32 337 17.3 363 2 Q6EN45  
33 335 17.2 243 2 Q8S3P1  
34 334.5 17.1 362 2 Q9ZPL9  
35 334.5 17.1 380 2 Q8S821  
36 333.5 17.1 371 2 Q8VZN9  
37 333.5 17.1 387 2 Q6L5H6  
38 332.5 17.0 359 2 Q82469  
39 332 17.0 283 2 Q8L7I4  
40 332 17.0 445 2 Q6L4R7  
41 329 16.9 339 2 Q757M1  
42 328 16.8 362 2 Q9ZW21  
43 326 16.7 307 2 Q9FGM3  
44 326 16.7 464 2 Q9FXE4  
45 325 16.7 281 1 P2C1\_YEAST

## ALIGNMENTS

RESULT 1  
Q8N3J5 PRELIMINARY; PRT; 372 AA.  
AC Q8N3J5  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 28, Last sequence update)  
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
DE Hypothetical protein DKF2p761G058 (protein phosphatase 2C kappa)  
DE (PP2C-like protein).  
GN Name=DKF2p761G058;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Amalgam;  
RG The German cDNA Consortium;  
RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RN Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
RL [2]  
RP SEQUENCE FROM N.A.  
RA Xu J., Stagliano N., Deponte J. III, Rodrigue-Way A., Golden S.,  
RA Katz S., Jeyaseelan R., Donoghue M., Meyers R., Gottfried S.,  
RA Wysong D., McGovern K., Pollman M., Breitbart R.E., Acton S.;  
RN Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RL [3]  
RP SEQUENCE FROM N.A.  
MAO Y., Xie Y., Dai J.;  
RT "Cloning and characterization of a novel human PP2C gene from fetal  
brain."  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
CC - SIMILARITY: Belongs to the PP2C family.  
DR EMBL; AL834271; CAD38946.1; -  
DR EMBL; AY435431; AAR06213.1; -  
DR EMBL; AV157615; AAO17296.1; -  
DR HSP; P35813; IAGQ.  
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000222; PP2C.  
DR InterPro; IPR001932; PP2C-like.  
DR Pfam; PF00481; PP2C; 1.  
DR PROSITE; PS01032; PP2C; 1.  
DR HydroLase; Hypothetical protein; Magnesium.  
SQ SEQUENCE 372 AA; 40997 MW; 9DD37EEC0EAD3313 CRC64;

Query Match 100.0%; Score 1951; DB 2; Length 372;

Best Local Similarity 100.0%; Pred. No. 4.5e-154; Indels 0; Gaps 0;

Matches 372; Conservative 0; Mismatches 0;

QY 1 MSTAALITLVRSQGNVRRRVLSSRLLODRRVTPVTCSTSEPRCSFRPDGSGSPAT 60

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Db      1 MSTAAITLTVRSQGNQVRRVLLSSRLQDDRRVPTCHSSSTSEPRCSRFPDGGSGSPAT 60
      61 WDNFGIWDNRIDEPILLPSIKYKGPPIKISLENVCASQIGKRKENEDRDFPAQLTDEV 120
Db      61 WDNFGIWDNRIDEPILLPSIKYKGPPIKISLENVCASQIGKRKENEDRDFPAQLTDEV 120
Qy      121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLPEKKNLETLTLTAFLIDKAFSSHARLSAD 180
Db      121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLPEKKNLETLTLTAFLIDKAFSSHARLSAD 180
Qy      181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db      181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Qy      241 GGFVAVNSLQGPVHGRLAMTSGIDLDLKTSGVIAEPETKRIKLHADDSDFLVLTDDGI 300
Db      241 GGFVAVNSLQGPVHGRLAMTSGIDLDLKTSGVIAEPETKRIKLHADDSDFLVLTDDGI 300
Qy      301 NFWVNSQEIICDFVNOCHDNEAAHVAHQIAIYGTEDNSTAVVVPFGANGKYKNSINFS 360
Db      301 NFWVNSQEIICDFVNOCHDNEAAHVAHQIAIYGTEDNSTAVVVPFGANGKYKNSINFS 360
Qy      361 FSRSPASSGRWA 372
Db      361 FSRSPASSGRWA 372

RESULT 2
Q96NT4 ID Q96NT4 PRELIMINARY; PRT; 372 AA.
AC Q96NT4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ30116.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RX PubMed=14702039; DOI=10.1038/ngl1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Oabayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosioki T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togliya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RA "Complete sequencing and characterization of 21,243 full-length human

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RT      CDNAS ";
RL      Nat. Genet. 36:40-45 (2004).
CC      -I- SIMILARITY: Belongs to the PP2C family.
DR      EMBL; AK054678; BAB7090.1; -.
DR      HSSP; P35813; 1A60.
DR      GO; GO:008287; C:protein serine/threonine phosphatase complex; IEA.
DR      GO; GO:0016787; F:hydrolase activity; IEA.
DR      GO; GO:000287; F:magnesium ion binding; IEA.
DR      GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR      GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR      InterPro; IPR001932; PP2C-like.
DR      InterPro; IPR002222; PP2C.
DR      Pfam; PF00481; PP2C; 1.
DR      SMART; SM00332; PP2C; 1.
DR      SMART; SM00331; PP2C-SIG; 1.
DR      PROSITE; PS01032; PP2C; 1.
KW      Hydrolase; Magnesium.
SQ      SEQUENCE 372 AA; 40983 MW; 7065B29DC79CB93B CRC64;

Query Match 99.9%; Score 1950; DB 2; Length 372;
Best Local Similarity 99.7%; Pred. No. 5.4e-154;
Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MSTAAITLTVRSQGNQVRRVLLSSRLQDDRRVPTCHSSSTSEPRCSRFPDGGSGSPAT 60
Db      1 MSTAAITLTVRSQGNQVRRVLLSSRLQDDRRVPTCHSSSTSEPRCSRFPDGGSGSPAT 60

Qy      61 WDNFGIWDNRIDEPILLPSIKYKGPPIKISLENVCASQIGKRKENEDRDFPAQLTDEV 120
Db      61 WDNFGIWDNRIDEPILLPSIKYKGPPIKISLENVCASQIGKRKENEDRDFPAQLTDEV 120

Qy      121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLPEKKNLETLTLTAFLIDKAFSSHARLSAD 180
Db      121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLPEKKNLETLTLTAFLIDKAFSSHARLSAD 180

Qy      181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db      181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

Qy      241 GGFVAVNSLQGPVHGRLAMTSGIDLDLKTSGVIAEPETKRIKLHADDSDFLVLTDDGI 300
Db      241 GGFVAVNSLQGPVHGRLAMTSGIDLDLKTSGVIAEPETKRIKLHADDSDFLVLTDDGI 300

Qy      301 NFWVNSQEIICDFVNOCHDNEAAHVAHQIAIYGTEDNSTAVVVPFGANGKYKNSINFS 360
Db      301 NFWVNSQEIICDFVNOCHDNEAAHVAHQIAIYGTEDNSTAVVVPFGANGKYKNSINFS 360

Qy      361 FSRSPASSGRWA 372
Db      361 FSRSPASSGRWA 372

RESULT 3
Q8IUZ7 ID Q8IUZ7 PRELIMINARY; PRT; 372 AA.
AC Q8IUZ7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp761G058.
GN Name=DKFZp761G058;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the PP2C family.  
 RA EMBL; AK044610; BAC32001.1; -.  
 DR HSP; P35813; IAG6.  
 DR MGD; MG1:2442111; A930026103Rik.  
 DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:000287; F:magnesium ion binding; IEA.  
 DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR001932; PP2C.  
 DR InterPro; IPR00222; PP2C.  
 DR Pfam; PF00481; PP2C; 1.  
 DR SMART; SM00332; PP2C; 1.  
 DR SMART; SM00331; PP2C SIG; 1.  
 DR PROSITE; PS01032; PP2C; 1.  
 DR Hydroxylase; Hypothetical protein; Magnesium.  
 KW SEQUENCE 372 AA; 40918 MW; 3749BEB94F211E7A CRC64;  
 SQ  
 Query Match 91.1%; Score 1777; DB 2; Length 372;  
 Best Local Similarity 90.3%; Pred. No. 1.4e-139;  
 Matches 336; Conservative 18; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVPTCHSTSEPRCSRPDPDGGSPAT 60  
 DB 1 MLSAAPTLLRSQGNQVKKVLLSSILLQDHRQATPACYPSTSEARCSRPDPDGGSPAT 60  
 QY 61 WDNFGIWNDRIDPILLPPSIKYKPIKISLENVGCASQIGKRNEDRDFPAQLTDEV 120  
 DB 61 WDNFGIWNDRIDPILLPPSIKYKPIKISLENVGCASLIGKRNEDRDFGPAQLTEV 120  
 QY 121 LYFAVVDHGGAADAFCHTHMEKCIIMDLIPKKNLETLITLAFIDKAFSSHARLSAD 180  
 DB 121 LYFAVVDHGGAADAFCHTHMEKCIIMDLIPKKNLETLITLAFIDKAFSAHLSAD 180  
 QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKPKMKLTDHTPERKDKERIKKC 240  
 DB 181 ASLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKPKMKLTDHTPERKDKERIKKF 240  
 QY 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSVIAPEPTKRIKLHADDPSFLVLTDDGI 300  
 DB 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSVIAPEPTKRIKLHADDPSFLVLTDDGI 300  
 QY 301 NFMVNSQIEICDFVNOCHDNPNEAAHATEQAIQYGTEDNSTAVVVPFGANGKYKNSIFTS 360  
 DB 301 NFMVNSQIEICDFVNOCHDNPNEAAHATEQAIQYGTEDNSTAVVVPFGANGKYKNSIFTS 360  
 QY 361 FSRSPASSGRWA 372  
 DB 361 FSRSPASSGRWA 372  
 RESULT 5  
 Q6ING9 PRELIMINARY; PRT; 373 AA.  
 AC Q6ING9  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE MGC82621 protein.  
 GN Names=MGC82621;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OC NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 Krzywinski M.I., Skalska J., Smallos D.E., Schnerch A., Schein J.E.,  
 Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RA Klein S., Strausberg R.;  
 CC Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the PP2C family.  
 DR EMBL; BC072312; AAH72312.1; -.  
 DR HSP; P35813; IAG6.  
 DR GO; GO:000287; C:protein serine/threonine phosphatase complex; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:000287; F:magnesium ion binding; IEA.  
 DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.  
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
 DR InterPro; IPR00222; PP2C.  
 DR InterPro; IPR001932; PP2C-like.  
 DR Pfam; PF00481; PP2C; 1.  
 DR SMART; SM00332; PP2C; 1.  
 DR SMART; SM00331; PP2C SIG; 1.  
 DR PROSITE; PS01032; PP2C; 1.  
 DR Hydroxylase; Magnesium.  
 KW SEQUENCE 373 AA; 41536 MW; 58713DIA52099BB7 CRC64;  
 SQ  
 Query Match 71.7%; Score 1399.5; DB 2; Length 373;  
 Best Local Similarity 72.1%; Pred. No. 4.2e-108;  
 Matches 269; Conservative 41; Mismatches 60; Indels 3; Gaps 2;  
 QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVPTCHSTSEPRC--SRFPDGGSGSP 58  
 DB 1 MSTAALVLLRNGRCQVNGA-LTLCFQKEHSTCTTTRHCFSANRRCSFRRFDDGSGRP 59  
 QY 59 ATWDFGIWNRIDEPILLPPSIKYKPIKISLENVGCASQIGKRNEDRDFPAQLTD 118  
 DB 60 ATWDSFGIWNDRIDEPILLPPSIKYKPIKISLENVGCSTQLGKRNEDRDFKARLTP 119  
 QY 119 EVLYFAVVDHGGAADAFCHTHMEKCIIMDLIPKKNLETLITLAFIDKAFSSHARLS 178  
 DB 120 DILYFAVVDHGGAADAFCHTHMEKCIIMDLIPKKNLETLITLAFIDKAFSSHARLS 179  
 QY 179 ADATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKPKMKLTDHTPERKDKERI 238  
 DB 180 VDASLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKPKMKLTDHTPERKDKERI 239  
 QY 239 KCGFVAVNSLQGVHNGRLAMTRISIGDLTKTSVIAPEPTKRIKLHADDPSFLVLTDD 298  
 DB 240 KSGGFVAVNSLQGVHNGRLAMTRISIGDLTKTSVIAPEPTKRIKLHADDPSFLVLTDD 299  
 QY 299 GINFMVNSQIEICDFVNOCHDNPNEAAHATEQAIQYGTEDNSTAVVVPFGANGKYKNSIN 358

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Db 300 GINFINVSEICDIINQCHDPKEAAQVLTEQAIOYGTEDNSTAIVVPFGAWGKHKSSEVS 359
Qy 359 FFSRSRFPASSGRW 371
Db 360 FFSRGRFPASSGRW 372

RESULT 6
Q81XG7 PRELIMINARY; PRT; 233 AA.
AC Q81XG7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE U0082E07.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mao Y., Xie Y.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the PP2C family.
DR EMBL; AF351614; AA76514.1; -.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium.
SQ SEQUENCE 233 AA; 25692 MW; EB90A7B3BC1BDD08 CRC64;

Query Match 48.8%; Score 951.5; DB 2; Length 233;
Best Local Similarity 86.6%; Pred. No. 5e-71;
Matches 187; Conservative 5; Mismatches 17; Indels 7; Gaps 1;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
Qy 61 WDNFGIWDNRIDEPILLPPSIKYKPIKISLENVGCASQIGRKENEDRDFPAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYKPIKISLENVGCASQIGRKENEDRDFPAQLTDEV 120
Qy 121 LYFAVYDGHGGAADFCFTHMEKICMDLLPKKKNLETLTLAFLFKAFSSSHARLSAD 180
Db 121 LYFAVYDGHGGAADFCFTHMEKICMDLLPKKKNLETLTLAFLFKAFSSSHARLSAD 180
Qy 181 ATLLTSGT-----TATVALLRDLGIELVWASVGDG 209
Db 181 ENCAWSAALDLFVDTICGASVEREICLLISQVKES 216

RESULT 7
Q8ND70 PRELIMINARY; PRT; 182 AA.
AC Q8ND70;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein DKFP667B084.
GN Name=DKFP667B084;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RC TRISSUE=Lymph node;
RA Ansoerge W., Winkner U., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the PP2C family.
DR EMBL; AL834167; CAD38869.1; -.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Hypothetical protein; Magnesium.
SQ SEQUENCE 182 AA; 20239 MW; 0D2523DE99A810BB CRC64;

Query Match 48.7%; Score 950; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 4.8e-71;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
Qy 61 WDNFGIWDNRIDEPILLPPSIKYKPIKISLENVGCASQIGRKENEDRDFPAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYKPIKISLENVGCASQIGRKENEDRDFPAQLTDEV 120
Qy 121 LYFAVYDGHGGAADFCFTHMEKICMDLLPKKKNLETLTLAFLFKAFSSSHARLSAD 180
Db 121 LYFAVYDGHGGAADFCFTHMEKICMDLLPKKKNLETLTLAFLFKAFSSSHARLSAD 180

RESULT 8
Q67UX7 PRELIMINARY; PRT; 348 AA.
AC Q67UX7;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein OSUNBa0050G13.3.
GN Name=OSUNBa0050G13.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
clone:OSUNBa0050G13."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005412; BAD38042.1; -.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hypothetical protein.
SQ SEQUENCE 348 AA; 37568 MW; 43405A0F8056495C CRC64;

Query Match 18.9%; Score 369; DB 2; Length 348;
Best Local Similarity 37.5%; Pred. No. 3.1e-22;
Matches 99; Conservative 48; Mismatches 85; Indels 32; Gaps 11;

Qy 96 GCASQIGRKENED-----RFDFAQLTDEVLYFAVYDGHGGAADFCFTHMEKICMDLLP 151
Db 84 GYASAPGKRAMSEDFYETRIDGVD-GETIGLFGVDGHGGAARAEYVKOHL---FSNLTK 139

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QY 152 KEK---NLETLLTLAFLEID----KAFSSHARLSADATLLTSGTTATVALLRDIQLVVA 204
D 140 HPKFIIDISAETYNHTDSEFLKAESHTR-----DAGSTASTAIL-VGDRLLVA 190
QY 205 SVGDSRAILCRGKPKMLTIDHTPERKDEKRIKCGGFVAMNSLQOPHVGSLAMTRSI 264
D 191 NVGDSRAVVCRGDAITAVSRDHKPDQDSRQRIEDAGGFVWM--AGTWRVGGVLAVSRAF 248
QY 265 GOLDLKTSGVIABPETYRIKLHHAADS--FLVTTDGINFMVNSQIICDFVNOCHDPNEA 322
D 249 GOKLLK-QYVADPE---IKEEIVDSLSLEFLILASDGLWDVNSKEADVVRPIQDPEQA 304
QY 323 AHAVTEQAIQYGTEDNSTAVVVPF 346
D 305 AKRLQEQYQSGADNITVVIVRF 328

RESULT 9
Q8LAY8 PRELIMINARY; PRT; 354 AA.
ID Q8LAY8 AC Q8LAY8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Protein phosphatase 2C-like protein (hypothetical protein
DE At5g10740/T30N20.10) (Hypothetical protein At5g10740).
GN Name=At5g10740/T30N20.10; Synonyms=At5g10740;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=22088475; Pubmed=12093376;
RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; genome
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RN Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [2]
RN SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA Nakajima M., Enju A., Kaniya A., Narusaka M., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kaniya A., Kawai J., Kim C.-O., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
CC -1- SIMILARITY: Belongs to the PP2C family.
DR EMBL; AY087522; AA65064.1; -.
DR EMBL; AK117549; BAC42210.1; -.
DR EMBL; BT005431; AAO63851.1; -.
DR HSSP; P35813; 1A6Q.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.

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DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C-SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 354 AA; 38036 MW; 87DA535B561C9D68 CRC64;

Query Match 18.9%; Score 369; DB 2; Length 354;
Best Local Similarity 36.1%; Pred. No. 3.2e-22;
Matches 101; Conservative 56; Mismatches 93; Indels 30; Gaps 11;

QY 96 GCASQIQGKKEKNEFRD--FAQLTDEVL-YFAVYDGHGGPAAADFCHTHWEKICIMDLPPK 152
D 35 GYASSAGKXSMEDFFETRIDGINGEIVGLFGVFDGCGGARAAYVKRHL---FSNLIITH 91
QY 153 EK---NLETLLTLAFLEID----KAFSSHARLSADATLLTSGTTATVALLRDIQLVVA 205
D 92 PKFISDTKSAITDAYNHTDSELLKSENHNR-----DAGSTASTAIL-VGDRLLVVA 142
QY 206 VGDSSRAILCRGKPKMLTIDHTPERKDEKRIKCGGFVAMNSLQOPHVGSLAMTRSI 265
D 143 VGDSSRAVTSRGKATAVSRDHKPDQDSRQRERENAGGFVWM--AGTWRVGGVLAVSRAF 200
QY 266 DLDLKTSGVIABPETYRIKLHHAADS--FLVTTDGINFMVNSQIICDFVNOCHDPNEA 323
D 201 DRLLK-QYVADPEQEEKI---DQTLLELILASDGLWDVFSNEAAVAVKVEDEPDSA 256
QY 324 HAVTEQAIQYGTEDNSTAVVVPFGAWGKYKNSEINFPSR 363
D 257 KKLVGGAIRKGSADNITCVVVRFLKKSSASSSHISSSK 296

RESULT 10
Q9LEW5 PRELIMINARY; PRT; 348 AA.
ID Q9LEW5 AC Q9LEW5
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protein phosphatase 2C-like protein.
GN Name=T30N20.10;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RA Bevan M., Peters S.A., van Staveren M., Dirkee W., Stiekema W.,
RA Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the PP2C family.
DR EMBL; AL365234; CAB96829.1; -.
DR PIR; T50783; T50783.
DR HSSP; P35813; 1A6Q.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C-SIG; 1.
DR SMART; SM00331; PP2C-SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
DR HydroLase; Magnesium.
SQ SEQUENCE 348 AA; 37379 MW; 12447BB07F740B2C CRC64;

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Query Match 18.5%; Score 360; DB 2; Length 348;  
Best Local Similarity 35.4%; Pred. No. 1.7e-21;  
Matches 99; Conservative 56; Mismatches 89; Indels 36; Gaps 11;

QY 96 GCASQIGKRNEDRPD--PAQLTDEVL--YFAYVDGHHGGAADFCFTHMEKIMDLPK 152  
DB 35 GYASSAGKSSMEDFPETRIDGNGIVGFVGDHGGGARAAYVKRHU---FSNLITH 91

QY 153 EK---NLETLTLTALFLAID----KAFSSSHARLSADATLTLTSGTTATVALLRDGIELVWAS 205  
DB 92 PKFISTKSAITDAYNHTDSELKSENHR-----DAGSTASTAIL-VGDRLLVAN 142

QY 206 VGDRAILCRKQKPKMLTIDHTPERKDEKRIKKCGFVAVNSLQGFVNHNGRLAMTRSIG 265  
DB 143 VGDRAVISRGGAIAVSRDHKPDQSDERERIEIENAGGVNM-----AGVLAVSRAPG 194

QY 266 DLDLKTSGVTAEPETKRIKLHADD--FLAVTTDGINFMVNSQICDFVNOCHDPNEAA 323  
DB 195 DRLLK-QYVVADPEIQEIKT---DQTLLEFLILASDGLWDVFSNEAAVAMVKEVEDPDSA 250

QY 324 HAYTEQAIOYGTEDNSTAVVVPFGAMGKYKNSEINFESFR 363  
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Q61V73  
ID O61V73 PRELIMINARY; PRT; 290 AA.  
AC O61V73  
DT 05-JUL-2004 (TEMBLrel. 27, Created)  
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)  
DE Protein phosphatase 2C.  
GN Name:PP2C;  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Xu Y., Li D., Gu L., Li D.;  
RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
RC -I- SIMILARITY: Belongs to the PP2C family.  
RL EMBL; AY621066; AAT40439.1; -.  
DR HSP; P35813; 1A6Q.  
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0000287; F:magnesium ion binding; IEA.  
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000222; PP2C.  
DR InterPro; IPR001932; PP2C-like.  
DR Pfam; PF00481; PP2C; 1.  
DR SMART; SM00332; PP2C; 1.  
DR SMART; SM00331; PP2C SIG; 1.  
DR PROSITE; PS01032; PP2C; 1.  
KW Hydrolase; Magnesium.  
SQ SEQUENCE 290 AA; 31193 MW; 6958PF6E6B44BBB CRC64;

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QY 152 KEK---NLETLTLTALFLAIDKAFSSSHARLSADAT-LTSGTTATVALLRDGIELVWASVG 207  
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QY 208 DRAILCRKQKPKMLTIDHTPERKDEKRIKKCGFVAVNSLQGFVNHNGRLAMTRSIGDL 267

DB 135 DSRVAVSKGGQGIASRDHKPDQTDERQIEDAGGFVMW--AGTWVGGVLAVSRAPGDK 192

QY 268 DLKTSVTAEPETKRIKLHADD--FLVTTDGINFMVNSQICDFVNOCHDPNEAAHA 325  
DB 193 LLKPY-VVADPE---IKEEVDSLSLEFLILASDGLWDVVTNEEAVAMVKIQDPOEANK 248

QY 326 VTEQAIOYGTEDNSTAVVVPF 346  
DB 249 LLEASRRGSSDNTIIVIRF 269

RESULT 12  
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ID Q9M1P8 PRELIMINARY; PRT; 383 AA.  
AC Q9M1P8  
DT 01-OCT-2000 (TEMBLrel. 15, Created)  
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)  
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)  
DE Hypothetical protein T17J13.220 (Protein phosphatase-2C).  
GN Name:T17J13.220;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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RN [1]  
RP SEQUENCE FROM N.A.  
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,  
RA Lemcke K., Mayer K.F.X., Quetier F., Salancubet M.;  
RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22088475; PubMed=12093376;  
RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,  
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
RT "Full-length messenger RNA sequences greatly improve genome  
RT annotation.";  
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL138651; CAB71886.1; -.  
DR EMBL; AY085949; AAM63159.1; -.  
DR PIR; T48018; T48018.  
DR HSP; P35813; 1A6Q.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR InterPro; IPR00222; PP2C.  
DR InterPro; IPR001932; PP2C-like.  
DR Pfam; PF00481; PP2C; 1.  
DR SMART; SM00332; PP2C; 1.  
DR SMART; SM00331; PP2C SIG; 1.  
DR PROSITE; PS01032; PP2C; UNKNOWN\_1.  
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QY 100 QIGKRKNEED---RFD-----FQALTDEVLYFAYVDGHHGGAADFCFTHMEKIMD 148  
DB 83 DIGPKRNMEDEHIRIDDLSSQVGSFLFELPKPSAFYAVFDGHHGGAAYVR---ENAIRF 139





Db 400 SKDNISVVVVVDLKGIRKPKSKSLN 423

Search completed: June 17, 2005, 00:57:06

Job time : 175 secs

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RT signal transduction."
RL Plant Cell 9:759-771(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RA Rodriguez P.L., Grill E.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RL MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:31-63(2000).
CC -!- FUNCTION: Involved in abscisic acid (ABA) signaling pathway.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SIMILARITY: Belongs to the PP2C family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y08966; CAA70163.1; -
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DR EMBL; Y11840; CAA72538.1; -
DR EMBL; AB024035; BAA97035.1; -
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DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2CC; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Calcium-binding; Hydrolase; Magnesium; Manganese; Multigene family;
KW Protein phosphatase.
FT CA_BIND 70 81 EF-hand (Potential).
SQ SEQUENCE 423 AA; 46306 MW; 67CAAC76DAS31A71 CRC64;

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Best Local Similarity 30.6%; Pred. No. 6.5e-21;
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QY 185 TSGTTATVALLRDGIELVWASVGSRAILCRKKGPKMLTIDHTPERKDEKERIKKCGG-F 243
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229 TVGSTSVAVVFP-THIFVANGDSRAVLCEGKTPFLSLSDVHKPDRDDEAARIEAAGKV 287
QY 244 VANNSLGQPHVNGRLAMTRSIGDLTKTSGVIAEPE---TKRIKLHHADDSFLVLTDDGI 300
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288 IRWNG---ARVFGVLAMSRSIGDRLKPS-VIPDPEVTSVRRVK---EDDCLILASDGL 339
QY 301 NFWVNSQEIICDFVNO-----CHDPN-----EAAHAVTEQAIQYG 334
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QY 335 TEDNSTAVVVPFGAWGKYKNSIN 358
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 17, 2005, 00:57:16 ; Search time 160 Seconds  
(without alignments)  
892.752 Million cell updates/sec

Title: US-10-716-489-2

Perfect score: 1951

Sequence: 1 MSTAALITLVRSGNQVRRR.....KNSINFSPSPASSGRWA 372

Scoring table: BLOSUM62

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Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1951	100.0	372	9	US-09-973-064-4
3	1951	100.0	372	9	US-09-973-077-4
4	1951	100.0	372	9	US-09-973-063-4
5	1951	100.0	372	9	US-09-973-964-4
6	1951	100.0	372	9	US-09-975-072-4
7	1951	100.0	372	9	US-09-972-038-4
8	1951	100.0	372	9	US-09-972-757-4
9	1951	100.0	372	9	US-09-973-965-4
10	1951	100.0	372	9	US-09-973-941-4
11	1951	100.0	372	10	US-09-986-992-2

12	1951	100.0	372	10	US-09-971-782-4	Sequence 4, Appli
13	1951	100.0	372	15	US-10-311-764-1	Sequence 1, Appli
14	1951	100.0	372	16	US-10-716-488-2	Sequence 2, Appli
15	1951	100.0	372	16	US-10-716-489-2	Sequence 2, Appli
16	1951	100.0	372	16	US-10-776-013-2	Sequence 2, Appli
17	1951	100.0	372	17	US-10-716-442-2	Sequence 2, Appli
18	1950	99.9	372	15	US-10-094-749-1699	Sequence 1699, Ap
19	1950	99.9	372	16	US-10-408-765A-2487	Sequence 2487, Ap
20	1924	88.6	373	9	US-09-925-300-1655	Sequence 1655, Ap
21	1727	88.5	352	9	US-09-860-351-2	Sequence 2, Appli
22	1727	88.5	352	15	US-10-353-690-44	Sequence 44, Appli
23	790	40.5	150	15	US-10-094-749-3238	Sequence 2238, Ap
24	412.5	21.1	260	15	US-10-072-012-853	Sequence 853, App
25	395.5	20.3	252	15	US-10-072-012-854	Sequence 854, App
26	370.5	19.0	300	9	US-09-801-267-4	Sequence 4, Appli
27	370.5	19.0	300	14	US-10-170-789-35	Sequence 35, Appli
28	369	18.9	348	16	US-10-437-963-164347	Sequence 164347, Ap
29	361	18.5	405	15	US-10-424-599-219801	Sequence 219801, Ap
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31	360	18.5	374	15	US-10-424-599-176581	Sequence 176581, Ap
32	359	18.4	371	15	US-10-425-114-66152	Sequence 66152, A
33	357.5	18.3	349	16	US-10-425-115-191052	Sequence 191052, A
34	356.5	18.3	345	15	US-10-425-114-66340	Sequence 66340, A
35	356	18.2	333	15	US-10-425-114-62820	Sequence 62820, A
36	356	18.2	348	16	US-10-425-115-232153	Sequence 232153, A
37	354.5	18.2	362	16	US-10-437-963-144908	Sequence 144908, Ap
38	354	18.1	405	16	US-10-425-115-275171	Sequence 275171, Ap
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41	353	18.1	370	15	US-10-425-114-69654	Sequence 69654, A
42	353	18.1	375	15	US-10-425-114-63857	Sequence 63857, A
43	350.5	18.0	360	15	US-10-168-506-21	Sequence 21, Appli
44	350.5	18.0	360	15	US-10-343-357-2	Sequence 2, Appli
45	350.5	18.0	360	17	US-10-838-181-21	Sequence 21, Appli

## ALIGNMENTS

RESULT 1  
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; Patent No. US20020106676A1  
; GENERAL INFORMATION:  
; APPLICANT: Roch, Jean-Marc  
; APPLICANT: Bartel, Paul L.  
; APPLICANT: Helchman, Karen  
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative  
; FILE REFERENCE: Protein Interactions in ND  
; CURRENT APPLICATION NUMBER: US/09/973,963  
; CURRENT FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: US 60/240,790  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: US 60/304,775  
; PRIOR FILING DATE: 2001-07-13  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-973-963-4

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RESULT 2
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; Patent No. US2002010673A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,064
; CURRENT FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-064-4

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RESULT 3
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; Patent No. US20020114799A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,077
; CURRENT FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-077-4

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QY 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLKTSGVIAEPETKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLKTSGVIAEPETKRIKLHHADDSFLVLTDDGI 300
QY 301 NFVNSQIEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAMGKYKNSEINFS 360
Db 301 NFVNSQIEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAMGKYKNSEINFS 360
QY 361 FRSFSPASSGRWA 372
Db 361 FRSFSPASSGRWA 372

RESULT 4
US-09-973-063-4
; Sequence 4, Application US/09973063
; Patent No. US20020115119A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
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Db 61 WDNFGIWDNRIDEPILLPSIKYKIPKISLENVGCASQIGRKKNEDRFDPAQLTDEV 120
QY 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLKTSGVIAEPETKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLKTSGVIAEPETKRIKLHHADDSFLVLTDDGI 300
QY 301 NFVNSQIEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAMGKYKNSEINFS 360
Db 301 NFVNSQIEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAMGKYKNSEINFS 360
QY 361 FRSFSPASSGRWA 372
Db 361 FRSFSPASSGRWA 372

RESULT 2
US-09-973-064-4
; Sequence 4, Application US/09973064
; Patent No. US2002010673A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,064
; CURRENT FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-064-4

Query Match 100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 1e-194;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNOVRRVLLSSRLQLQDDRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60
Db 1 MSTAALITLVRSGNOVRRVLLSSRLQLQDDRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPSIKYKIPKISLENVGCASQIGRKKNEDRFDPAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPSIKYKIPKISLENVGCASQIGRKKNEDRFDPAQLTDEV 120
QY 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLKTSGVIAEPETKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLKTSGVIAEPETKRIKLHHADDSFLVLTDDGI 300
QY 301 NFVNSQIEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAMGKYKNSEINFS 360
Db 301 NFVNSQIEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAMGKYKNSEINFS 360
QY 361 FRSFSPASSGRWA 372
Db 361 FRSFSPASSGRWA 372

RESULT 3
US-09-973-077-4
; Sequence 4, Application US/09973077
; Patent No. US20020114799A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,077
; CURRENT FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-077-4

Query Match 100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 1e-194;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNOVRRVLLSSRLQLQDDRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60
Db 1 MSTAALITLVRSGNOVRRVLLSSRLQLQDDRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPSIKYKIPKISLENVGCASQIGRKKNEDRFDPAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPSIKYKIPKISLENVGCASQIGRKKNEDRFDPAQLTDEV 120
QY 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLKTSGVIAEPETKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLKTSGVIAEPETKRIKLHHADDSFLVLTDDGI 300
QY 301 NFVNSQIEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAMGKYKNSEINFS 360
Db 301 NFVNSQIEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVVPFGAMGKYKNSEINFS 360
QY 361 FRSFSPASSGRWA 372
Db 361 FRSFSPASSGRWA 372

RESULT 4
US-09-973-063-4
; Sequence 4, Application US/09973063
; Patent No. US20020115119A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
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Matches	372;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
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Dd	1	MSTAALITLVRSGNQVRRRVLLSSRLQLDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT	60						
Qy	61	WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASOIGRKENEDRFDFPAQLTDEV	120						
Dd	61	WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASOIGRKENEDRFDFPAQLTDEV	120						
Qy	121	LYFAVDYGHGGPAAADFCHTHMEKCIMDLLLPKEKNLETLLTLAFLEIDKAFSSHARLSAD	180						
Dd	121	LYFAVDYGHGGPAAADFCHTHMEKCIMDLLLPKEKNLETLLTLAFLEIDKAFSSHARLSAD	180						
Qy	181	ATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKLTIIDHTPERKDEKERIKKC	240						
Dd	181	ATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKLTIIDHTPERKDEKERIKKC	240						
Qy	241	GGFVANNSLGOPHVNGELAMTRISIGDDLKTSGVIAPEPTKRILKHHADDSEFLVLTDDGI	300						
Dd	241	GGFVANNSLGOPHVNGELAMTRISIGDDLKTSGVIAPEPTKRILKHHADDSEFLVLTDDGI	300						
Qy	301	NFWNSOEICDFVNOCHDPNEAAHVAHQTEQAIOYGTEDNSTAVVPFGAWGKYKNSEINFS	360						
Dd	301	NFWNSOEICDFVNOCHDPNEAAHVAHQTEQAIOYGTEDNSTAVVPFGAWGKYKNSEINFS	360						
Qy	361	FRSFASFSSGRWA	372						
Dd	361	FRSFASFSSGRWA	372						
<b>RESULT 6</b>									
US-09-975-072-4									
; Sequence 4, Application US/09975072									
; Patent No. US20020115607A1									
; GENERAL INFORMATION:									
; APPLICANT: Roch, Jean-Marc									
; APPLICANT: Bartel, Paul L.									
; APPLICANT: Heichman, Karen									
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative									
; DISEASES									
; FILE REFERENCE: Protein Interactions in ND									
; CURRENT APPLICATION NUMBER: US/09/975,072									
; CURRENT FILING DATE: 2001-10-12									
; PRIOR APPLICATION NUMBER: US 60/240,790									
; PRIOR FILING DATE: 2000-10-17									
; NUMBER OF SEQ ID NOS: 4									
; SOFTWARE: PatentIn ver. 2.0									
; SEQ ID NO 4									
; LENGTH: 372									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-975-072-4									
Query Match									
Best Local Similarity 100.0%; Score 1951; DB 9; Length 372;									
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0									
Qy	1	MSTAALITLVRSGNQVRRRVLLSSRLQLDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT	60						
Dd	1	MSTAALITLVRSGNQVRRRVLLSSRLQLDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT	60						
Qy	61	W							

Qy	241	GGFVAVNSLQPHVNGRLAMTRISIGDLDLKTSVIAETPETKRIKLUHHADDSFLVLT	300
Db	241	GGFVAVNSLQPHVNGRLAMTRISIGDLDLKTSVIAETPETKRIKLUHHADDSFLVLT	300
Qy	301	NFMVNSQEI CDPVNQCHDPNEAAHAHVTSQA IQYGTEDNSTAVVVPFGAWGKYKNGSEINFS	360
Db	301	NFMVNSQEI CDPVNQCHDPNEAAHAHVTSQA IQYGTEDNSTAVVVPFGAWGKYKNGSEINFS	360
Qy	361	FSRSFASGRWA	372
Db	361	FSRSFASGRWA	372

RESULT 7  
US-09-972-038-4  
; Sequence 4, Application US/09972038  
; Patent No. US20020119155A1  
; GENERAL INFORMATION:  
; APPLICANT: Roch, Jean-Marc  
; APPLICANT: Bartel, Paul L.  
; APPLICANT: Heichman, Karen  
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative  
; TITLE OF INVENTION: Diseases  
; FILE REFERENCE: Protein Interactions in ND  
; CURRENT APPLICATION NUMBER: US/09/972,038  
; CURRENT FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: US 60/240,790  
; PRIOR FILING DATE: 2000-10-17  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-972-038-4

RESULT 8  
US-09-372-757-4  
; Sequence 4, Application US/09972757

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; Patent No. US2002011927A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/972,757
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-972-757-4

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RESULT 9
; US-09-973-965-4
; Sequence 4, Application US/09973965
; Patent No. US20020124273A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,965
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4

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; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-965-4

Query Match      100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 1e-194;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRDPDGGSGSPAT 60
Db 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRDPDGGSGSPAT 60

Qy 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKKENEDRFDFAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKKENEDRFDFAQLTDEV 120

Qy 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKENLETLTLTFLAFLEIDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKENLETLTLTFLAFLEIDKAFSSHARLSAD 180

Qy 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

Qy 241 GGFVANNISLQOPHNGRLAMTRISIGDLKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300
Db 241 GGFVANNISLQOPHNGRLAMTRISIGDLKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300

Qy 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360

Qy 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 10
US-09-973-941-4
; Sequence 4, Application US/09973941
; Patent No. US20020164655A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,941
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-941-4

Query Match      100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 1e-194;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRDPDGGSGSPAT 60
Db 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRDPDGGSGSPAT 60

Qy 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKKENEDRFDFAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKKENEDRFDFAQLTDEV 120
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Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKKENEDRFDFAQLTDEV 120
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Db 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKENLETLTLTFLAFLEIDKAFSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Qy 241 GGFVANNISLQOPHNGRLAMTRISIGDLKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300
Db 241 GGFVANNISLQOPHNGRLAMTRISIGDLKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300
Qy 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Qy 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 11
US-09-986-992-2
; Sequence 2, Application US/09986992
; Publication No. US20030027308A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN PHOSPHATASES IDENTIFIED FROM
; TITLE OF INVENTION: GENOMIC SEQUENCING
; FILE REFERENCE: 038602/1277
; CURRENT APPLICATION NUMBER: US/09/986,992
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/246,974
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/208,291
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-992-2

Query Match      100.0%; Score 1951; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 1e-194;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRDPDGGSGSPAT 60
Db 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRDPDGGSGSPAT 60

Qy 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGRKKENEDRFDFAQLTDEV 120
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Qy 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKENLETLTLTFLAFLEIDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKENLETLTLTFLAFLEIDKAFSSHARLSAD 180

Qy 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

Qy 241 GGFVANNISLQOPHNGRLAMTRISIGDLKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300
Db 241 GGFVANNISLQOPHNGRLAMTRISIGDLKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300

Qy 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
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Db 301 NFMVNSQEIFVFNQCHDPAEAHAHVAEQAIQGTEDNSTAVVVPFGAMGKYKNSEINFS 360  
 QY 361 FSRSPASSGRWA 372  
 Db 361 FSRSPASSGRWA 372

RESULT 12  
 US-09-971-782-4  
 ; Sequence 4, Application US/09971782  
 ; Publication No. US20030186317A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Roch, Jean-Marc  
 ; APPLICANT: Bartel, Paul L.  
 ; APPLICANT: Heichman, Karen  
 ; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative  
 ; FILE REFERENCE: Protein Interactions in ND  
 ; CURRENT APPLICATION NUMBER: US/09/971,782  
 ; CURRENT FILING DATE: 2001-10-09  
 ; PRIOR APPLICATION NUMBER: US 60/240,790  
 ; PRIOR FILING DATE: 2000-10-17  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 372  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-971-782-4

Query Match 100.0%; Score 1951; DB 10; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 1e-194;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 MSTAALITLVRSGNQVRRVLLSRLLQDDRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60  
 QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRFDPAQLTDEV 120  
 Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRFDPAQLTDEV 120  
 QY 121 LYFAVVDGHHGGAADPFCHTHMEKCIIMDLPPKKNLETLTLTFLAFIDKAFSSHARLSAD 180  
 Db 121 LYFAVVDGHHGGAADPFCHTHMEKCIIMDLPPKKNLETLTLTFLAFIDKAFSSHARLSAD 180  
 QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
 Db 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
 QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDKTSGVIAEPETKRIKLHADDPSFLVLTDDGI 300  
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 QY 301 NFMVNSQEIFVFNQCHDPAEAHAHVAEQAIQGTEDNSTAVVVPFGAMGKYKNSEINFS 360  
 Db 301 NFMVNSQEIFVFNQCHDPAEAHAHVAEQAIQGTEDNSTAVVVPFGAMGKYKNSEINFS 360  
 QY 361 FSRSPASSGRWA 372  
 Db 361 FSRSPASSGRWA 372

RESULT 13  
 US-10-311-764-1  
 ; Sequence 1, Application US/10311764  
 ; Publication No. US20040023245A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.  
 ; APPLICANT: BAUGHN, Mariah R.; DING, Li  
 ; APPLICANT: ELLIOTT, Vicki S.; GANDHI, Ameena R.  
 ; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.

; APPLICANT: KEARNEY, Liam; LEE, Ernestine A.  
 ; APPLICANT: LU, Yan; NGUYEN, Damiel B.  
 ; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi  
 ; APPLICANT: REDDY, Roopa M.; SANOJANWALA, Madhusudan M.  
 ; APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom  
 ; APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.  
 ; APPLICANT: CHAWLA, Narinder K.; YANG, Junming  
 ; APPLICANT: YAO, Monique G.; YUE, Henry  
 ; TITLE OF INVENTION: PROTEIN PHOSPHATASES  
 ; FILE REFERENCE: PI-0126 USN  
 ; CURRENT APPLICATION NUMBER: US/10/311,764  
 ; CURRENT FILING DATE: 2002-12-16  
 ; PRIOR APPLICATION NUMBER: PCT/US01/19442  
 ; PRIOR FILING DATE: 2001-06-14  
 ; PRIOR APPLICATION NUMBER: US 60/212,447  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/213,746  
 ; PRIOR FILING DATE: 2000-06-22  
 ; PRIOR APPLICATION NUMBER: US 60/215,210  
 ; PRIOR FILING DATE: 2000-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/216,529  
 ; PRIOR FILING DATE: 2000-07-06  
 ; PRIOR APPLICATION NUMBER: US 60/218,080  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/220,117  
 ; PRIOR FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 1  
 ; LENGTH: 372  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US20040023245A1 8124196CD1  
 US-10-311-764-1

Query Match 100.0%; Score 1951; DB 15; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 1e-194;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSTAALITLVRSGNQVRRVLLSRLLQDDRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60  
 Db 1 MSTAALITLVRSGNQVRRVLLSRLLQDDRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60  
 QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRFDPAQLTDEV 120  
 Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRFDPAQLTDEV 120  
 QY 121 LYFAVVDGHHGGAADPFCHTHMEKCIIMDLPPKKNLETLTLTFLAFIDKAFSSHARLSAD 180  
 Db 121 LYFAVVDGHHGGAADPFCHTHMEKCIIMDLPPKKNLETLTLTFLAFIDKAFSSHARLSAD 180  
 QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
 Db 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
 QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDKTSGVIAEPETKRIKLHADDPSFLVLTDDGI 300  
 Db 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDKTSGVIAEPETKRIKLHADDPSFLVLTDDGI 300  
 QY 301 NFMVNSQEIFVFNQCHDPAEAHAHVAEQAIQGTEDNSTAVVVPFGAMGKYKNSEINFS 360  
 Db 301 NFMVNSQEIFVFNQCHDPAEAHAHVAEQAIQGTEDNSTAVVVPFGAMGKYKNSEINFS 360  
 QY 361 FSRSPASSGRWA 372  
 Db 361 FSRSPASSGRWA 372

RESULT 14  
 US-10-716-488-2  
 ; Sequence 2, Application US/10716488





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2005, 00:50:20 ; Search time 42 Seconds  
(without alignments)  
661.177 Million cell updates/sec

Title: US-10-716-489-2

Perfect score: 1951

Sequence: 1 MSTAALITLVRSGNQVRRR.....KNSINFSRSPASSGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1951	100.0	372	4	US-09-973-963-4
2	325	16.7	281	2	US-08-822-701-9
3	325	16.7	281	3	US-08-935-855-9
4	325	16.7	281	4	US-08-935-855-9
5	319.5	16.4	390	2	US-08-873-093-3
6	319.5	16.4	390	4	US-09-206-646-3
7	314	16.1	392	3	US-09-013-881-2
8	314	16.1	392	4	US-09-612-473-2
9	314	16.1	392	4	US-09-724-730-2
10	307.5	15.8	382	4	US-09-538-092-1086
11	307.5	15.8	382	4	US-09-949-016-6982
12	307.5	15.8	390	4	US-09-206-646-4
13	307.5	15.8	458	4	US-09-949-016-7534
14	306.5	15.7	306	3	US-08-822-701-8
15	306.5	15.7	306	2	US-08-935-855-8
16	300	15.4	309	2	US-08-822-701-7
17	300	15.4	309	3	US-08-935-855-7
18	294.5	15.1	353	4	US-09-828-302-14
19	290.5	14.9	454	4	US-09-538-092-1156
20	282.5	14.5	478	2	US-08-873-093-1
21	282.5	14.5	478	2	US-08-873-093-4
22	282.5	14.5	479	4	US-09-206-646-1
23	282.5	14.5	479	4	US-09-949-016-11294
24	281.5	14.4	387	4	US-09-461-325-178
25	281.5	14.4	387	4	US-10-012-542-178
26	281.5	14.4	387	4	US-10-115-123-178
27	279	14.3	314	2	US-08-822-701-10

28	279	14.3	314	3	US-08-935-855-10	Sequence 10, Appl
29	277.5	14.2	335	4	US-09-270-767-43565	Sequence 43565, A
30	264	13.5	386	4	US-09-248-796A-18312	Sequence 18312, A
31	261.5	13.4	241	4	US-09-270-767-32790	Sequence 32790, A
32	261.5	13.4	241	4	US-09-270-767-48007	Sequence 48007, A
33	231	11.8	669	4	US-09-270-767-46055	Sequence 46055, A
34	228.5	11.7	542	3	US-08-935-855-22	Sequence 22, Appl
35	228	11.7	553	4	US-09-949-016-7397	Sequence 7397, Ap
36	226	11.6	546	3	US-08-935-855-20	Sequence 20, Appl
37	226	11.6	546	4	US-09-538-092-827	Sequence 827, App
38	226	11.6	546	4	US-09-949-016-6265	Sequence 6265, Ap
39	223	11.4	392	2	US-08-822-701-2	Sequence 2, Appli
40	223	11.4	392	3	US-08-935-855-2	Sequence 2, Appli
41	222	11.4	345	4	US-09-248-796A-14637	Sequence 14637, A
42	219	11.2	626	4	US-09-949-016-8097	Sequence 8097, Ap
43	214	11.0	286	4	US-09-270-767-61602	Sequence 61602, A
44	203	10.4	695	4	US-09-248-796A-18020	Sequence 18020, A
45	202.5	10.4	393	4	US-09-538-092-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-09-973-963-4

; Sequence 4, Application US/09973963

; Patent No. 6653102

; GENERAL INFORMATION:

; APPLICANT: Roch, Jean-Marc

; APPLICANT: Bartel, Paul L.

; APPLICANT: Heichman, Karen

; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative

; TITLE OF INVENTION: Diseases

; FILE REFERENCE: Protein Interactions in ND

; CURRENT APPLICATION NUMBER: US/09/973,963

; CURRENT FILING DATE: 2001-10-11

; PRIOR APPLICATION NUMBER: US 60/240,790

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: US 60/304,775

; PRIOR FILING DATE: 2001-07-13

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 4

; LENGTH: 372

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-973-963-4

Query Match 100.0%; Score 1951; DB 4; Length 372;

Best Local Similarity 100.0%; Pred. No. 7e-193;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSTAALITLVRSGNQVRRVLLSSRLLODDRVTPTCHSSTSEPCRSRDPDGGSPAT	60
Db	1	MSTAALITLVRSGNQVRRVLLSSRLLODDRVTPTCHSSTSEPCRSRDPDGGSPAT	60
Qy	61	WDNFGIWDNRIDRPIPPSIKYGKPIPKISLENVGCSAIOIGKRNEDRDFQAQLTDEV	120
Db	61	WDNFGIWDNRIDRPIPPSIKYGKPIPKISLENVGCSAIOIGKRNEDRDFQAQLTDEV	120
Qy	121	LYFVYDGHGPGAAADFCHTHMEKIMDLPKKNLETLTLTAFLEIDKAFSSHARLSAD	180
Db	121	LYFVYDGHGPGAAADFCHTHMEKIMDLPKKNLETLTLTAFLEIDKAFSSHARLSAD	180
Qy	181	ATLTSGTATTALLRDGIELVWASVGDSSRAILCRKQPKMLTTDHTPERKDEKIKKC	240
Db	181	ATLTSGTATTALLRDGIELVWASVGDSSRAILCRKQPKMLTTDHTPERKDEKIKKC	240
Qy	241	GGFVWNSLQPHVNGRLAMTRISGDLDLKTSVGIARPETKRIKLHADDLSFLVLTDDGI	300
Db	241	GGFVWNSLQPHVNGRLAMTRISGDLDLKTSVGIARPETKRIKLHADDLSFLVLTDDGI	300
Qy	301	NFMVNSQEI CDFVNOCHDPNEAAHVAHQEQAIQYGTEDNSTAVVVPFGAWGKYKNSINF	360



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QY      344 V 344
DB      279 V 279

RESULT 4
US-09-538-092-91
; Sequence 91, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; FILE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; TITLE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormat Version 0.9
; SEQ ID NO 91
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number YDL006W
US-09-538-092-91

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Query Match      16.7%; Score 325; DB 4; Length 281;
Best Local Similarity 32.8%; Pred. No. 5.1e-25;
Matches 79; Conservative 48; Mismatches 82; Indels 32; Gaps 7;

QY      122 YFAVDGCHGPPAAADFCHTHMEKIMD--LLPKKNELETLTLAFLAIDKAFSGSHARLSA 179
DB      53 YFAVFDGAGIQASKWCGKHLHTIEQNILADETRDVRDVLNDSFLAIDEINT----- 106

QY      180 DATLLTSGTTATVALLR-----DGI-----ELVVASVGDSSRAILCRKPKMKLT 223
DB      107 -KLVNGSGCTAAVCLRWELPDSVSDSDMLAQHQKLYTANVGDSRI VLFENGNSIRLT 165

QY      224 IDHTPERKDEKERIKKCGFVAMNSLQPHVNGELATRSIGDLDLKTSGVIAEPETKRI 283
DB      166 YDHKASDTLEMQRVEQAGGLIM-----KSRVNGMLAVTRSLGD-KFFDSLWVGSPFTTSV 219

QY      284 KLHHADDSFLVLTDDGINFMVNSOEICDFVNOCHDPNEAAHVAHQEAIQYGTEDNSTAVV 343
DB      220 EI-TSEDKFLLACDGLWDVDDQACELIKDITEPNEAAKLVRYALENGTTDNTVTVW 278

QY      344 V 344
DB      279 V 279

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RESULT 5
US-08-873-093-3
; Sequence 3, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive

```

```

; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1247927
; US-08-873-093-3

Query Match      16.4%; Score 319.5; DB 2; Length 390;
Best Local Similarity 31.6%; Pred. No. 3.2e-24;
Matches 94; Conservative 48; Mismatches 108; Indels 47; Gaps 10;

QY      88 PKISLENV-----GCASQIGKREKEDR----FDFALQTLDEVLYFAVYDGHGPPAA 134
DB      8 PKTEKINAHGAGNGLRYGLSSMQGWRVEMEDATVAVVGIPHGLEDSWFFFAVYDGHGSRV 67

QY      135 ADPCHTM-----EKIMDLLPKKNELETLTLAFLAIDKAFSGSHARLSADA 181
DB      68 ANYCSTHLEHITTNEFDRAADKSGFALEPSVENVTGRTGFLKIDSYMRNFSDLRNG- 126

QY      182 TLTSGTTATVALLRDLGIELVVASVGDSSRAILCRKPKMKLTIDHTPERKDEKERIKKCG 241
DB      127 -MDRSGSTA-VGVMISPTHYFINGGDSRAVLCRNGQVCFSTQDHKPCNPKERIQWAG 184

QY      242 GFVAMNSLQPHVNGRLAMTRISIGDLDLK-----TSGVIA-EPETKRIKLHHADDSFL 293
DB      185 G-----SVMTQRVNGSLAVSRALGDYDKVDGKGPTQLVSPPEVVEI-LRAEDEFV 238

QY      294 VLTTDGINFMVNSOEICDFVNO-----CHDNEAAHVAHQEAIQYGTEDNSTAVVVPF 346
DB      239 VLACDGIWVMSNEELCEFNRSRLVSDLDLENVNCNVVVDTCCLKHKSRRDNMSIVLCF 295

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RESULT 6
US-09-206-646-3
; Sequence 3, Application US/09206646
; Patent No. 6436637
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; FILE REFERENCE: PF-0319-1 DIV
; CURRENT APPLICATION NUMBER: US/09/206,646
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4

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; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: ID No. 6436637 g247927
US-09-206-646-3

Query Match      16.4%; Score 319.5; DB 4; Length 390;
Best Local Similarity 31.6%; Pred. No. 3.2e-24;
Matches 94; Conservative 48; Mismatches 108; Indels 47; Gaps 10;

QY 88 PKISLENV-----GCASQIGKKNEDR-----FDFALQTLDEVLVYFVYDGHGPPAA 134
Db 8 PKTEKNAHGAGNGLRYGLSSMQGRVEMEDAHTAVVGIPHGLEDSFFFAVYDGHAGSRV 67
QY 135 ADFCHTHM-----EKCIMDLLPEKNLETLTLFLAFLEIDKAFSSHARLSADA 181
Db 68 ANYCSTHLEHITNEDFRAADKSGFALESVENVTGINTGFLKIDEYMRNFSDLANG- 126
QY 182 TLTSGTTATVALLRDIELVAVSGDSRAILCRKGKPKMLTIDHTPERKDEKERIKKCG 241
Db 127 -MDRSGSTA-VGWMISPTHYIFINCDSRAVLCRNGQVCFSTQDHPKPCNPMKERIQNAG 184
QY 242 GFVAVNSLGOPHVNGLAMTRSRIGDLDLK-----TSGVIA-EPETKRIKLHADDSPFL 293
Db 185 G-----SVMTQVNGSLAVSRALGDYDKVDGKGPTQLVSPPEYVEI-LRAEEDFV 238
QY 294 VLTTDGINFMVNSQIECDFVQ-----CHDPNEAAHVAEQAIQYGTEDNSTAVVVPF 346
Db 239 VLACDGIWVNSNEELCEFFVNSRLEVSDDLENVCNVVDTCLHKGGRDNMSIVLVCF 295

RESULT 7
US-09-013-881-2
; Sequence 2, Application US/09013881
; Patent No. 6132964
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,881
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0470 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT02
; CLONE: 195647
US-09-013-881-2

Query Match      16.1%; Score 314; DB 3; Length 392;
Best Local Similarity 27.5%; Pred. No. 1.2e-23;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

QY 27 LQDDRVRVPTCHSSTSEPRCSRDPDGGSGPATWNFGIWNRIDEPILLPSI----- 81
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QY 82 -----KYG-----KPIPKISLENVGASQIGKKN-ENED 109
Db 61 SLATSISQMVKTEGKAKRKTSEEEKNGSEELVEKKVCRASSVIFGLKGYVAERKGEREE 120
QY 110 RPD-----FAQLTDE-----VLVYFVYDGHGPPAAADFCHTHMEKCIMDLLPK--- 152
Db 121 MQDAHVILNDITEECRPPSSLIITRVSYFAVFDGGHGRASKFAAQNHLHQLIRKFPKGDV 180
QY 153 ----EKNLETLTLAFLEIDKAFSSHARLSADATLTLTSGTTATVALLRDIELVAVSGDS 209
Db 181 ISVEKTVKCLLDTFKHTDEEFLKQA--SSQKPAWKGSGTATCVLAVDNI-LYIANLGDS 237
QY 210 RAILCR-----KXKPMKLTIDHTPERKDEKERIKKCGGFVAVNSLGOPHVNGLAMTRSR 263
Db 238 RAILCRYNESOKHAALSLSKEHNPTOYERMRIQKAGG-----NVRDGRVLGVLEVSRS 292
QY 264 IGDLDLKTSGVTAEPETKRIKLHADDSPFLVLTDDGINFMVNSQIECDFVNOCHDPNE-- 321
Db 293 IGDQYKRCGVTSVPDIRRQCL--TPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQ 351
QY 322 -----AAHVAEQAIQYGTEDNSTAVVVPFG 347
Db 352 TREKSAADARYEAACNRLANKAVQSGADNVTVVVRIG 391

RESULT 8
US-09-612-473-2
; Sequence 2, Application US/09612473
; Patent No. 6518029
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; FILE REFERENCE: PF-0470-1 CIP
; CURRENT APPLICATION NUMBER: US/09/612,473
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/013,881
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6518029 195647
US-09-612-473-2
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASES, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-04-14

; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-10-20

; PRIOR FILING DATE: 2000-10-03  
; PRIOR FILING DATE: 2000-10-03

; PRIOR FILING DATE: 2000-09-08  
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 6982  
; LENGTH: 382

; TYPE: PRT  
; ORGANISM: Human

US-09-949-016-6982

Query Match 15.8%; Score 307.5; DB 4; Length 382;  
Best Local Similarity 31.0%; Pred. No. 5.3e-23;

Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;

Qy 88 PKISLENV-----GCASQIGKRENER-----PDFAQLTDEVLYFVYDGHGGPAA 134

Db 8 PKMEKNAQGGNGLRYGLSSMOGWVEMEDAHAVIGLPSGLSWFSFVAYDGHAGSQV 67

Qy 135 ADFCHTHM-----ERKIMDLPEKKNLETLTLLAFLEIDKAPFSSSHARLSADA 181

Db 68 AKYCEHLLDHTNNQDFKGSAGAPSVENVKNGIRTGFTGFLDEHMRVMEKKHGD--- 123

Qy 185 TSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKCGFV 244

Db 124 RSGSTA-VGVLSPOHTYFINGCDGSRGLLCRNKRVHFFTDHKKPSNPLEKERNAGG-- 180

Qy 245 AMNSLGOPHVNGLAMTRSGDLDLK-----TSGVIA-EPETKRIKLHADDSEFLVLT 296

Db 181 ---SVMIQRVNGSLAVSRALGDFYKCVHGKPTQELVSPPEVHDIERSEEDDQFIILA 237

Qy 297 TDGINFMVNSQIECDFVNO-----CHDPNEAAHVAITEQAIQYGTEDNSTAVVVPF 346

Db 238 CDGIWDMGNEELCDFVRSRLVETDLDLEKVCNEVVDTCLYKGRDNMSVILICF 291

RESULT 12

US-206-646-4

; Sequence 4, Application US/09206646

; Patent No. 6436637

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Goli, Surya K.

; APPLICANT: Lal, Preeti G.

; APPLICANT: Corley, Neil C.

; APPLICANT: Zhang, Hong

; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE

; FILE REFERENCE: PP-0319-1 DIV

; CURRENT APPLICATION NUMBER: US/09/206,646

; CURRENT FILING DATE: 2001-12-07

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PERL Program

; SEQ ID NO 4

; LENGTH: 390

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: ID No. 6436637 9452526

US-09-206-646-4

Query Match 15.8%; Score 307.5; DB 4; Length 390;  
Best Local Similarity 31.0%; Pred. No. 5.5e-23;

Matches 92; Conservative 48; Mismatches 110; Indels 47; Gaps 10;

Qy 88 PKISLENV-----GCASQIGKRENER-----PDFAQLTDEVLYFVYDGHGGPAA 134

Db 8 PKMEKNAQGGNGLRYGLSSMOGWVEMEDAHAVIGLPSGLSWFSFVAYDGHAGSQV 67

Qy 135 ADFCHTHM-----ERKIMDLPEKKNLETLTLLAFLEIDKAPFSSSHARLSADA 181

Db 68 ANYCSTHLLHEHTTNEEDFRAADKSGSALEPVSVEKGTGRTGFLKIDVYMRNFSDLRNG- 126

Qy 182 TLTGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKCG 241

Db 127 -MDRSGSTA-VGVVSPHTMYFINGCDGSRGLLCRNKRVHFFTDHKKPSNPLEKERNAG 184

Qy 242 GFVAMNSLGOPHVNGLAMTRSGDLDLK-----TSGVIA-EPETKRIKLHADDSEFL 293

Db 185 G-----SVMIQRVNGSLAVSRALGDFYKCVHGKPTQELVSPPEVYEI-VRAEDEFV 238

Qy 294 VLTGGINFMVNSQIECDFVNO-----CHDPNEAAHVAITEQAIQYGTEDNSTAVVVPF 346

Db 239 VLACDGIWDMGNEELCDFVRSRLVETDLDLEKVCNEVVDTCLYKGRDNMSVILICF 295

RESULT 13

US-09-949-016-7534

; Sequence 7534, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7534

; LENGTH: 458

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-7534

Query Match 15.8%; Score 307.5; DB 4; Length 458;  
Best Local Similarity 31.0%; Pred. No. 7.1e-23;

Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;

Qy 88 PKISLENV-----GCASQIGKRENER-----PDFAQLTDEVLYFVYDGHGGPAA 134

Db 84 PKMEKNAQGGNGLRYGLSSMOGWVEMEDAHAVIGLPSGLSWFSFVAYDGHAGSQV 143

Qy 135 ADFCHTHMCKIMDL-----LPKEKLETLTLLAFLEIDK--AFSSSHARLSADATLL 184

Db 144 AKYCEHLLDHTNNQDFKGSAGAPSVENVKNGIRTGFTGFLDEHMRVMEKKHGD---- 199

Qy 185 TSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKCGFV 244

Db 200 RSGSTA-VGVLSPOHTYFINGCDGSRGLLCRNKRVHFFTDHKKPSNPLEKERNAG-- 256

Qy 245 AMNSLGOPHVNGLAMTRSGDLDLK-----TSGVIA-EPETKRIKLHADDSEFLVLT 296

Db 257 ---SVMIQRVNGSLAVSRALGDFYKCVHGKPTQELVSPPEVHDIERSEEDDQFIILA 313

Qy 297 TDGINFMVNSQIECDFVNO-----CHDPNEAAHVAITEQAIQYGTEDNSTAVVVPF 346

Db 314 CDGIWDMGNEELCDFVRSRLVETDLDLEKVCNEVVDTCLYKGRDNMSVILICF 367

RESULT 14

US-08-822-701-8



```
; Sequence 8, Application US/08822701
; Patent No. 5976853
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,701
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Rattus
; US-08-822-701-8

Query Match 15.7%; Score 306.5; DB 2; Length 306;
Best Local Similarity 31.0%; Pred. No. 4.8e-23;
Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;

Qy 88 PKISLENV-----GCASQIGKRKENEDR----FDFAQLTDEVLYFAYVYDGHGGPAA 134
Db 8 PKMEKHNAQGGNGRLRYGLSSMOGWRVEMEDAHTAVIGLPSGLTWSFFAVYDGHAGSQV 67
Qy 135 ADFCHTHMEKICMDL-----LPKEKNLETLTLTFLAFLDK--AFSSSHARLSADATLL 184
Db 68 AKYCCHELLDHI TNQDFKGSAGAPSVENKNGIRTGTGLEIDEHMRVMSKKHGAD---- 123
Qy 185 TSGTTATVALLRGIELVVASVGSRAILCRKGPKMLTIDHTPERKDEKERIKKCGGFV 244
Db 124 RSGSTA-VGVLLSPQHTYFINGDSRGLLCNRKRVHFFFTQDKPSNPLEKERIQWAG-- 180
Qy 245 AwnSLGQPHVNGRLAMTFSIGDLK-----TSGVIA-EPETKRIKLHHADDSFLVLT 296
Db 181 ---SVMTQRVNGSLAVSRALGDFDKVHGKGPTEQLVSPPEVHDIERSEDDQFIILA 237
Qy 297 TDGINFMVNSOEICDFVNO-----CHDNEAAHAYTEQAIQYGTEDNSTAVVVPF 346
Db 238 CDGIWDVNGNEELCDFVRSRLVETDDLEKVCNEVVDTCLYKGRDNNMSVILICF 291
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RESULT 15

US-08-935-855-8

; Sequence 8, Application US/08935855

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; Patent No. 6066485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,855
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Rattus
; US-08-935-855-8

Query Match 15.7%; Score 306.5; DB 3; Length 306;
Best Local Similarity 31.0%; Pred. No. 4.8e-23;
Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;

Qy 88 PKISLENV-----GCASQIGKRKENEDR----FDFAQLTDEVLYFAYVYDGHGGPAA 134
Db 8 PKMEKHNAQGGNGRLRYGLSSMOGWRVEMEDAHTAVIGLPSGLTWSFFAVYDGHAGSQV 67
Qy 135 ADFCHTHMEKICMDL-----LPKEKNLETLTLTFLAFLDK--AFSSSHARLSADATLL 184
Db 68 AKYCCHELLDHI TNQDFKGSAGAPSVENKNGIRTGTGLEIDEHMRVMSKKHGAD---- 123
Qy 185 TSGTTATVALLRGIELVVASVGSRAILCRKGPKMLTIDHTPERKDEKERIKKCGGFV 244
Db 124 RSGSTA-VGVLLSPQHTYFINGDSRGLLCNRKRVHFFFTQDKPSNPLEKERIQWAG-- 180
Qy 245 AwnSLGQPHVNGRLAMTFSIGDLK-----TSGVIA-EPETKRIKLHHADDSFLVLT 296
Db 181 ---SVMTQRVNGSLAVSRALGDFDKVHGKGPTEQLVSPPEVHDIERSEDDQFIILA 237
Qy 297 TDGINFMVNSOEICDFVNO-----CHDNEAAHAYTEQAIQYGTEDNSTAVVVPF 346
Db 238 CDGIWDVNGNEELCDFVRSRLVETDDLEKVCNEVVDTCLYKGRDNNMSVILICF 291
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Search completed: June 17, 2005, 00:58:39

Job time : 44 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2005, 00:38:39 ; Search time 163 Seconds  
(without alignments)  
882.668 Million cell updates/sec

Title: US-10-716-489-2

Perfect score: 1951

Sequence: 1 MSTAAALITLVRSGGNQVRRR.....KNSINFSPSPASSGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1980s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1951	100.0	372	5	AAE23954 PN7740 pr
2	1951	100.0	372	5	Abb79999 Human pho
3	1951	100.0	372	5	Abg70789 Fe65 inte
4	1951	100.0	372	5	AAE23953 PN7740 pr
5	1951	100.0	372	5	Abg70801 Fe65 inte
6	1951	100.0	372	5	Abg70826 Fe65 inte
7	1951	100.0	372	5	Abb07402 Human pro
8	1951	100.0	372	5	AAE23976 Human PN7
9	1951	100.0	372	5	AAE24078 Human PN7
10	1951	100.0	372	5	AAE14451 Human pro
11	1951	100.0	372	6	Abu10309 Human pro
12	1951	100.0	372	6	AAO23055 Human ser
13	1951	100.0	372	7	Adb66824 Human PN7
14	1951	100.0	372	7	Adg73452 Novel hum
15	1951	100.0	372	8	Adq14718 Human pro
16	1951	100.0	372	8	Adr30806 Human ser
17	1950	99.9	372	6	Ada54131 Human pro
18	1950	99.9	372	7	Adj70681 Human hea
19	1950	99.9	372	8	Adn05534 Antipsori
20	1939	99.4	373	4	Aau22334 Novel hum
21	1924	98.6	373	3	Ab57077 Human pro
22	1921	98.5	404	8	Abm83874 Human dia
23	1809	92.7	351	5	Abb07401 Human pro
24	1777	91.1	372	7	Adf53640 Murine ph
25	1727	88.5	352	5	Abb78059 Amino aci

## ALIGNMENTS

### RESULT 1

AAE23954  
ID AAE23954 standard; protein; 372 AA.

XX AAE23954;

DT 23-SEP-2002 (first entry)

DE PN7740 protein.

XX Protein-protein interaction; neurodegenerative disorder; dementia;  
XX Huntington's disease; Parkinson's disease; Alzheimer's disease; AD;  
XX protein therapy; drug screening.

XX Unidentified.

XX WO200233114-A2.

XX 25-APR-2002.

PF 16-OCT-2001; 2001WO-US032199.

PR 17-OCT-2000; 2000US-0240790P.

XX (MYRI-) MYRIAD GENETICS INC.

XX Roch J, Bartel PL, Heichman K;

XX WPI; 2002-454603/48.

XX N-PSDB; AAD38600.

PT New protein complexes involved in neurodegenerative diseases, useful for  
PT diagnosing the presence of or a predisposition to a neurodegenerative  
PT disorders (e.g. Alzheimer's) or in screening for drugs for treating the  
PT diseases.

PS Example 6; Page 52; 93pp; English.

XX The invention relates to the discovery of protein-protein interactions  
XX that are involved in the pathogenesis of neurodegenerative disorders,  
XX including Alzheimer's disease (AD). The invention is also directed to  
XX protein complexes involved in neurodegenerative disorders. The protein  
XX complexes are useful for diagnosing the presence of or a predisposition  
XX to neurodegenerative disorders (e.g. Huntington's disease, Parkinson's  
XX disease, dementia and Alzheimer's disease). They are also useful in drug  
XX screening. The invention is used in protein therapy. The present sequence  
XX is PN7740 protein. This sequence is used in the exemplification of the  
XX invention

Ade31687 Human 161  
Abb07392 Human pro  
Abg06716 Novel hum  
Abg28412 Novel hum  
Aam41604 Human pol  
Aab47431 Human pro  
Aam39818 Human pol  
Ada55670 Human pro  
Abb07393 Human pro  
Abb07397 Human pro  
Adi17317 Polypepti  
Adi17318 Polypepti  
Aag06997 Arabidops  
Aag09824 Arabidops  
Adn73999 Thale cre  
Aae01345 Arabidops  
Abb07400 Amino aci  
Aae04841 Human SGP  
Aau75784 Human pro  
Abb78060 Consensus

26 1727 88.5 352 7 ADE31687  
27 1538.5 78.9 373 5 ABB07392  
28 1375.5 70.5 1072 4 ABG06716  
29 1375.5 70.5 1195 4 ABG28412  
30 1150 58.9 238 4 AAM41604  
31 951.5 48.8 233 4 AAB47431  
32 814 41.7 153 4 AAM39818  
33 790 40.5 150 6 ADA55670  
34 669.5 34.3 156 5 ABB07393  
35 437 22.4 83 5 ABB07397  
36 412.5 21.1 260 5 ADI17317  
37 395.5 20.3 252 5 ADI17318  
38 369 18.9 354 3 AAG06997  
39 357 18.3 383 3 AAG09824  
40 357 18.3 383 8 ADN73999  
41 354.5 18.2 423 4 AAE01345  
42 354.5 18.2 423 5 ABB07400  
43 350.5 18.0 360 4 AAE04841  
44 350.5 18.0 360 5 AAU75784  
45 350 17.9 274 5 ABB78060

XX SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;  
Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60  
DB 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEDRFDFAQLTDEV 120  
DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEDRFDFAQLTDEV 120

QY 121 LYPAVDGHHGPPAAADFCHTHMEKCIIMDLLPKENLETLTLAFLEIDKAFSSHARLSAD 180  
DB 121 LYPAVDGHHGPPAAADFCHTHMEKCIIMDLLPKENLETLTLAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAVNSLQPHVNGRLAMTRISIGDLTKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300  
DB 241 GGFVAVNSLQPHVNGRLAMTRISIGDLTKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300

QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360  
DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360

QY 361 FSRSFASSGRWA 372  
DB 361 FSRSFASSGRWA 372

RESULT 2  
ABB79999 standard; protein; 372 AA.

XX ABB79999;  
XX AC ABB79999;  
XX DT 19-DEC-2002 (first entry)  
XX DE Human phosphatase PN7740.  
XX KW PN7740; phosphatase; enzyme; human neurodegenerative disease;  
XX KW Alzheimer's disease; dementia; Parkinson's disease; Huntington's disease;  
XX KW diagnosis; therapy.  
XX OS Homo sapiens.

XX Key Location/Qualifiers  
XX Domain 104..339  
XX FT /note= "phosphatase 2C domain"  
XX FT

XX US2002115607-A1.  
XX PD 22-AUG-2002.  
XX PF 12-OCT-2001; 2001US-00975072.  
XX PR 17-OCT-2000; 2000US-0240790P.  
XX PA (MYRI-) MYRIAD GENETICS INC.  
XX PI Roch J, Bartel PL, Heichman K;  
XX DR WPI; 2002-722778/78.  
XX DR N-PSDB; ABQ81507.  
XX PT New protein complex useful for treating neurodegenerative disease e.g.  
XX PT Alzheimer's, comprises two proteins or their fragments, for e.g. BA13

PT with glypican, LRP2, LRPAP1 or transthyretin.  
PS Example 2-33; Page 23; 41pp; English.  
XX The present sequence is the protein sequence of a novel human  
CC phosphatase, designated PN7740. The sequence is predicted from a human  
CC brain cDNA clone identified in a yeast two-hybrid screening using as bait  
CC a fragment of Fe65 protein (amino acids 360-552, i.e. the first  
CC phosphotyrosine binding domain (PTB)). Identification of a phosphatase 2C  
CC domain showed PN7740 to be a novel phosphatase that binds to the first  
CC PTB of Fe65. Pharmacological modulation of this interaction may influence  
CC amyloid beta protein precursor metabolism. The invention provides protein  
CC complexes, identified by yeast two-hybrid screening, that comprise 2  
CC interacting proteins (or fragments), antibodies to the complexes,  
CC diagnosis of neurodegenerative disorders (including diagnosis of a  
CC predisposition to, or existence of, the disorder), drug screening for  
CC agents which modulate the protein interaction, and identification of  
CC additional proteins in the pathway common to the interacting proteins. A  
CC claimed method for treating a neurodegenerative disorder selected from  
CC Huntington's disease, Parkinson's disease, dementia and Alzheimer's  
CC disease involves administering a compound capable of modulating the  
CC protein complex. The compound may interfere with the protein interaction,  
CC bind one of the 2 proteins, may be an antibody immunoreactive with one of  
CC the proteins, or a nucleic acid encoding such an antibody, or is a  
CC compound that modulates expression of one of the proteins, is an  
CC antisense compound or ribozyme which hybridises to a nucleic acid  
CC encoding one of the proteins, or is a compound capable of strengthening  
CC the protein interaction (all claimed)  
XX SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;  
Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60  
DB 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEDRFDFAQLTDEV 120  
DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEDRFDFAQLTDEV 120

QY 121 LYPAVDGHHGPPAAADFCHTHMEKCIIMDLLPKENLETLTLAFLEIDKAFSSHARLSAD 180  
DB 121 LYPAVDGHHGPPAAADFCHTHMEKCIIMDLLPKENLETLTLAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAVNSLQPHVNGRLAMTRISIGDLTKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300  
DB 241 GGFVAVNSLQPHVNGRLAMTRISIGDLTKTSVIAEPETKRIKLHADDSEFLVLTDDGI 300

QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360  
DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360

QY 361 FSRSFASSGRWA 372  
DB 361 FSRSFASSGRWA 372

RESULT 3  
ABG70789  
ID ABG70789 standard; protein; 372 AA.  
XX ABG70789;  
XX AC ABG70789;  
XX DT 12-DEC-2002 (first entry)  
XX DE Fe65 interacting human protein, PN7740, protein.

XX Yeast two-hybrid; PN7740; human; CIB; calcium-binding protein; MLK2;  
 KW mixed lineage kinase 2; ligand; transporter; cellular uptake;  
 KW neuronal death; neurodegenerative disorder; Huntington's disease;  
 KW Parkinson's disease; dementia; Alzheimer's disease; APP; presenilin; PS1;  
 KW PS2; Abeta; trophic; sAPP; metabolite; Fe65.  
 OS Homo sapiens.  
 XX  
 XX US20021119927-A1.  
 XX  
 XX 29-AUG-2002.  
 XX  
 XX 09-OCT-2001; 2001US-00972757.  
 XX  
 XX 17-OCT-2000; 2000US-0240790P.  
 PR  
 XX (MYRI-) MYRIAD GENETICS INC.  
 XX  
 XX Roch J, Bartel PL, Heichman K;  
 XX  
 XX WPI; 2002-740204/80.  
 DR N-PSDB; ABS55204.  
 DR  
 XX  
 XX Modulating protein complex having proteins which is CIB interacting with  
 PT mixed lineage kinase 2, in a cell, by administering compound that  
 PT modulates the complex, or peptide that interferes interaction between  
 PT proteins.  
 PT  
 XX Example 6; Page 22; 37pp; English.  
 PS  
 XX The invention discloses a method for modulating in a cell, a protein  
 CC complex having a first protein, which is CIB (Calcium-binding protein),  
 CC interacting with a second protein, which is mixed lineage kinase (MLK)2,  
 CC or the interaction of MLK2 with the ligand, which comprises administering  
 CC to the cell a compound capable of modulating the protein complex or the  
 CC interaction, or a peptide capable of interfering with the protein's  
 CC interactions. The peptide is associated with a transporter capable of  
 CC increasing cellular uptake of the peptide. The method is useful for  
 CC modulating neuronal death in a patient having a neurodegenerative  
 CC disorder such as Huntington's disease, Parkinson's disease, dementia and  
 CC Alzheimer's disease. The technique used to discover additional proteins  
 CC that interact with the major Alzheimer's disease proteins (including APP,  
 CC not defined, and presenilins) was the yeast two-hybrid system. CIB has  
 CC been shown to interact with the presenilins, PS1 and PS2, but due to the  
 CC casual role of mutations of these presenilins in Alzheimer's disease,  
 CC other proteins, like MLK2, are likely to play a major role in the  
 CC pathogenesis. APP metabolism is also a critical event in Alzheimer's  
 CC or trophic (sAPP) metabolites. Fe65 (not defined) has been shown to  
 CC interact with APP and peptides interacting with Fe65 may also be useful  
 CC in treating neurodegenerative disorders. The compound may be capable of  
 CC strengthening the interaction between the first and the second protein.  
 CC The sequence presented is the human PN7740 protein which was isolated due  
 CC to its interaction with Fe65 found using the yeast two-hybrid system  
 XX  
 XX Sequence 372 AA;  
 SQ  
 Query Match 100.0%; Score 1951; DB 5; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MSTAALITLVRSQGNVRRVLLSRLLQDRRTPTCHSSTSPRCRSPFDDGSGSPAT 60  
 Db 1 MSTAALITLVRSQGNVRRVLLSRLLQDRRTPTCHSSTSPRCRSPFDDGSGSPAT 60  
 Qy 61 WDNFGIWNDRIDEPIPLPPSIKYGKPIPKISLENVGASQIGKKENEDRDFQAQLTDEV 120  
 Db 61 WDNFGIWNDRIDEPIPLPPSIKYGKPIPKISLENVGASQIGKKENEDRDFQAQLTDEV 120  
 Qy 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKENLETLLTFLAFLDKAFSSHARLSAD 180  
 Db 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKENLETLLTFLAFLDKAFSSHARLSAD 180

Qy 181 ATLLTSGTTATVALLRDGIELVVASVSDSRAILCRGKPKMLTIDHTPERKDEKERIKKC 240  
 Db 181 ATLLTSGTTATVALLRDGIELVVASVSDSRAILCRGKPKMLTIDHTPERKDEKERIKKC 240  
 Qy 241 GGFVAVNSLQOPHVNGRLAMTRISIGDLDLKTSQVIAPEPKRIKLIHHADDSFLVLTDDGI 300  
 Db 241 GGFVAVNSLQOPHVNGRLAMTRISIGDLDLKTSQVIAPEPKRIKLIHHADDSFLVLTDDGI 300  
 Qy 301 NFWNSOEICDFVNOCHDPNEAAHVAHQTEQAIQYGTEDNSTAVVVPFGAWGKYKXSEINFS 360  
 Db 301 NFWNSOEICDFVNOCHDPNEAAHVAHQTEQAIQYGTEDNSTAVVVPFGAWGKYKXSEINFS 360  
 Qy 361 FRSFASSGRWA 372  
 Db 361 FRSFASSGRWA 372  
 RESULT 4  
 AAE23953  
 ID AAE23953 standard; protein; 372 AA.  
 XX  
 AC AAE23953;  
 XX  
 DT 23-SEP-2002 (first entry)  
 XX  
 DE PN7740 protein.  
 XX  
 KW Protein-protein interaction; neurodegenerative disorder; CIB; MLK2;  
 KW Alzheimer's disease; calcium binding protein; mixed lineage kinase 2;  
 KW Huntington's disease; dementia; Parkinson's disease; AD.  
 XX  
 OS Unidentified.  
 XX  
 EN W0200233112-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 16-OCT-2001; 2001WO-US032196.  
 XX  
 PR 17-OCT-2000; 2000US-0240790P.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX  
 PI Roch J, Bartel PL, Heichman K;  
 XX  
 DR WPI; 2002-454607/48.  
 DR N-PSDB; AAD38594.  
 XX  
 PT New protein complex comprising CIB and mixed lineage kinase 2, useful as  
 PT targets for diagnostic tools in identifying individuals at risk for  
 PT neurodegenerative disorders, e.g. Alzheimer's disease, Parkinson's  
 PT disease or dementia.  
 XX  
 PS Example 6; Page 52; 91pp; English.  
 XX  
 CC The invention relates to the discovery of protein-protein interactions  
 CC that are involved in the pathogenesis of neurodegenerative disorders  
 CC including Alzheimer's disease (AD). The invention is also directed to  
 CC protein complex comprising two proteins selected from a complex of  
 CC calcium binding protein (CIB) and mixed lineage kinase 2 (MLK2). AD  
 CC interacting proteins are useful as new targets for the identification of  
 CC useful pharmaceuticals, new targets for diagnostic tools in the  
 CC identification of individuals at risk, sequences for producing  
 CC transformed cell lines, cellular models and animal models and new bases  
 CC for therapeutic intervention in neurodegenerative disorders, including.  
 CC Modulators of the protein complex are useful for treating  
 CC neurodegenerative disorders including Huntington's disease, dementia,  
 CC Parkinson's disease and AD. The present sequence is PN7740 protein. This  
 CC sequence used in the exemplification of the invention  
 XX  
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206; Mismatches 0; Indels 0; Gaps 0;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSNGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60  
 DB 1 MSTAALITLVRSNGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLNVGCSQIGRKKENEDRFDFAQLTDEV 120  
 DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLNVGCSQIGRKKENEDRFDFAQLTDEV 120

QY 121 LYFAVVDGHHGGAADFCCHTMEKCIIMDLLPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180  
 DB 121 LYFAVVDGHHGGAADFCCHTMEKCIIMDLLPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRGKPKMKLTIDHTPERKDKERIKKC 240  
 DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRGKPKMKLTIDHTPERKDKERIKKC 240

QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDLKTSQVIAEPETPKRIKLHADDSEFLVLTDDGI 300  
 DB 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDLKTSQVIAEPETPKRIKLHADDSEFLVLTDDGI 300

QY 301 NFVNSQEIICDFVNOCHDPNEAAHVAHQVTEQAIQYGTEDNSTAVVVPFGAMGKYKNSINF 360  
 DB 301 NFVNSQEIICDFVNOCHDPNEAAHVAHQVTEQAIQYGTEDNSTAVVVPFGAMGKYKNSINF 360

QY 361 FSRSPASSGRWA 372  
 DB 361 FSRSPASSGRWA 372

RESULT 5  
 ABG70801 ID ABG70801 standard; protein; 372 AA.  
 XX AC ABG70801;  
 DT 16-DEC-2002 (first entry)  
 XX Fe65 interacting human protein, PN7740, protein.  
 XX Yeast two-hybrid; PN7740; human; Mint2; PDE-9A; KIAA0427; ligand;  
 KW transporter; cellular uptake; neuronal death; neurodegenerative disorder;  
 KW Huntington's disease; Parkinson's disease; dementia; Alzheimer's disease;  
 KW APP; presenilin; Abeta; trophic; sAPP; metabolite; Fe65.  
 XX Homo sapiens.  
 XX US2002114799-A1.  
 XX 22-AUG-2002.  
 XX 10-OCT-2001; 2001US-00973077.  
 XX 17-OCT-2000; 2000US-0240790P.  
 XX (MYRI-) MYRIAD GENETICS INC.  
 XX Roch J, Bartel PL, Heichman K;  
 XX WPI; 2002-740090/80.  
 DR N-PSDB; ABS55222.  
 XX Modulating protein complex having Mint2 interacting with PDE-9A, by  
 PT administering compound capable of modulating protein complex, or peptide  
 PT capable of interfering with protein-protein interaction.  
 XX Example 6; Page 22; 37pp; English.  
 XX The invention discloses a method for modulating in a cell, a protein  
 CC complex having a first protein, which is Mint2, interacting with a second

CC protein, which is PDE-9A, or the interaction of PDE-9A with the ligand,  
 CC which comprises administering to the cell a compound capable of  
 CC modulating the protein complex or the interaction, or a peptide capable  
 CC of interfering with the protein's interactions. The peptide is associated  
 CC with a transporter capable of increasing cellular uptake of the peptide.  
 CC The method is useful for modulating neuronal death in a patient having a  
 CC neurodegenerative disorder such as Huntington's disease, Parkinson's  
 CC disease, dementia and Alzheimer's disease. The technique used to discover  
 CC additional proteins that interact with the major Alzheimer's disease  
 CC proteins (including APP, not defined, and presenilins) was the yeast two-  
 CC hybrid system. Mint2 has been shown to interact with APP, and due to its  
 CC interaction with presenilins and KIAA0427 it is likely to play a major  
 CC role in the pathogenesis of Alzheimer's disease. APP metabolism is also a  
 CC critical event in Alzheimer's disease pathogenesis as it leads to the  
 CC release of either toxic (Abeta) or trophic (sAPP) metabolites. Fe65 (not  
 CC defined) has been shown to interact with APP and peptides interacting  
 CC with Fe65 may also be useful in treating neurodegenerative disorders. The  
 CC compound may be capable of strengthening the interaction between the first  
 CC and the second protein. The sequence presented is the human PN7740  
 CC protein which was isolated due to its interaction with Fe65 found using  
 CC the yeast two-hybrid system  
 XX  
 SQ Sequence 372 AA;  
 Query Match 100.0%; Score 1951; DB 5; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206; Mismatches 0; Indels 0; Gaps 0;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSNGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60  
 DB 1 MSTAALITLVRSNGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLNVGCSQIGRKKENEDRFDFAQLTDEV 120  
 DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLNVGCSQIGRKKENEDRFDFAQLTDEV 120

QY 121 LYFAVVDGHHGGAADFCCHTMEKCIIMDLLPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180  
 DB 121 LYFAVVDGHHGGAADFCCHTMEKCIIMDLLPKEKNETLLTFLAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRGKPKMKLTIDHTPERKDKERIKKC 240  
 DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRGKPKMKLTIDHTPERKDKERIKKC 240

QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDLKTSQVIAEPETPKRIKLHADDSEFLVLTDDGI 300  
 DB 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDLKTSQVIAEPETPKRIKLHADDSEFLVLTDDGI 300

QY 301 NFVNSQEIICDFVNOCHDPNEAAHVAHQVTEQAIQYGTEDNSTAVVVPFGAMGKYKNSINF 360  
 DB 301 NFVNSQEIICDFVNOCHDPNEAAHVAHQVTEQAIQYGTEDNSTAVVVPFGAMGKYKNSINF 360

QY 361 FSRSPASSGRWA 372  
 DB 361 FSRSPASSGRWA 372

RESULT 6  
 ABG70826 ID ABG70826 standard; protein; 372 AA.  
 XX AC ABG70826;  
 XX 17-DEC-2002 (first entry)  
 XX Fe65 interacting human protein, PN7740, protein.  
 XX Yeast two-hybrid; PN7740; human; CIB; calcium-binding protein; MK2;  
 KW mixed lineage kinase 2; ligand; transporter; cellular uptake;  
 KW neuronal death; neurodegenerative disorder; Huntington's disease;  
 KW Parkinson's disease; dementia; Alzheimer's disease; APP; presenilin; PS1;  
 KW PS2; Abeta; trophic; sAPP; metabolite; Fe65.



Query Match 100.0%; Score 1951; DB 5; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDPDGGSPAT 60  
 DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDPDGGSPAT 60

QY 61 WDNFGIWNDRIDEPILLPSIKYKPIPKISLENVGCASQIGKRKENEDRFPDPAQLTDEV 120  
 DB 61 WDNFGIWNDRIDEPILLPSIKYKPIPKISLENVGCASQIGKRKENEDRFPDPAQLTDEV 120

QY 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180  
 DB 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAVNSLGQPHVNGRLAWTRSIGDLDLKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300  
 DB 241 GGFVAVNSLGQPHVNGRLAWTRSIGDLDLKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300

QY 301 NFWNSQEIICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGANGKYKNSINF 360  
 DB 301 NFWNSQEIICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGANGKYKNSINF 360

QY 361 FSRSPASSGRWA 372  
 DB 361 FSRSPASSGRWA 372

RESULT 8  
 AAE23976  
 ID AAE23976 standard; protein; 372 AA.  
 XX AAE23976;  
 AC AAE23976;  
 XX AAE23976;  
 DT 23-SEP-2002 (first entry)  
 DE Human PN7740 protein.  
 XX Human; protein-protein interaction; neurodegenerative disorder;  
 KW Alzheimer's disease; AD; pharmaceutical; Huntington's disease;  
 KW Parkinson's disease; anticonvulsant; dementia; neuroprotective;  
 KW nootropic; PN7740.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO200233113-A2.  
 XX 25-APR-2002.  
 XX 16-OCT-2001; 2001WO-US032197.  
 XX 17-OCT-2000; 2000US-0240790P.  
 XX (MYRI-) MYRIAD GENETICS INC.  
 XX Roch J, Bartel PL, Heichman K;  
 PI WPI; 2002-454608/48.  
 XX N-PSDB; AAD38691.  
 XX New protein complex comprising Mint2 and PDE-9A proteins, useful as  
 PT targets for diagnostic tools in identifying individuals at risk for  
 PT neurodegenerative disorders, e.g. Alzheimer's disease, Parkinson's  
 PT disease, or dementia.  
 XX Example 6; Page 52; 91pp; English.

CC The invention relates to the discovery of protein-protein interactions  
 CC that are involved in the pathogenesis of neurodegenerative disorders,  
 CC including Alzheimer's disease (AD). The AD interacting proteins are  
 CC useful as new targets for the identification of useful pharmaceuticals,  
 CC new targets for diagnostic tools in the identification of individuals at  
 CC risk, sequences for producing transformed cell lines, cellular models and  
 CC animal models, and new bases for therapeutic intervention in  
 CC neurodegenerative disorders, particularly AD. The DNA encoding the  
 CC protein of the invention can be used to create animals that overexpress  
 CC the protein, or animals which do not express the native gene but express  
 CC the protein. Modulators of the protein complex are useful for treating a  
 CC neurodegenerative disorder including Huntington's disease, Parkinson's  
 CC disease, dementia or Alzheimer's disease. The present sequence is human  
 CC PN7740 protein used in the exemplification of the invention  
 XX Sequence 372 AA;  
 SQ

Query Match 100.0%; Score 1951; DB 5; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDPDGGSPAT 60  
 DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDPDGGSPAT 60

QY 61 WDNFGIWNDRIDEPILLPSIKYKPIPKISLENVGCASQIGKRKENEDRFPDPAQLTDEV 120  
 DB 61 WDNFGIWNDRIDEPILLPSIKYKPIPKISLENVGCASQIGKRKENEDRFPDPAQLTDEV 120

QY 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180  
 DB 121 LYFAVVDGHHGGAADFCCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240  
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAVNSLGQPHVNGRLAWTRSIGDLDLKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300  
 DB 241 GGFVAVNSLGQPHVNGRLAWTRSIGDLDLKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300

QY 301 NFWNSQEIICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGANGKYKNSINF 360  
 DB 301 NFWNSQEIICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGANGKYKNSINF 360

QY 361 FSRSPASSGRWA 372  
 DB 361 FSRSPASSGRWA 372

RESULT 9  
 AAE24078  
 ID AAE24078 standard; protein; 372 AA.  
 XX AAE24078;  
 AC AAE24078;  
 XX AAE24078;  
 DT 04-OCT-2002 (first entry)  
 DE Human PN7740 protein.  
 XX Human; protein-protein interaction; neurodegenerative disorder;  
 KW Alzheimer's disease; AD; pharmaceutical; Huntington's disease;  
 KW Parkinson's disease; anticonvulsant; dementia; neuroprotective;  
 KW nootropic; PN7740.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO200232286-A2.  
 XX 25-APR-2002.  
 XX 16-OCT-2001; 2001WO-US032186.  
 XX 17-OCT-2000; 2000US-0240790P.



PR 13-JUL-2001; 2001US-0304775P.  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX  
 XX Roch J, Bartel PL, Reichman K;  
 PI  
 XX WPI; 2002-479640/51.  
 DR N-PSDB; AAD39176.  
 XX  
 XX Novel isolated protein complex having a protein which is postsynaptic  
 PT density protein or Fe65 interacting with another protein which is PN7740  
 PT useful for drug designing for treating neurodegenerative disorder.  
 XX  
 XX Claim 24; Page 52; 102pp; English.  
 XX  
 CC The invention relates to an isolated protein complex having a first  
 CC protein which is postsynaptic density protein (PSD95) or Fe65 interacting  
 CC with a second protein which is PN7740. Protein complex of the invention  
 CC is useful for diagnosing a neurodegenerative disorder in human, for  
 CC determining a predisposition to the neuro- degenerative disorder or for  
 CC the existence of the disorder. They are used for treating degenerative  
 CC disorders such as Huntington's disease, Parkinson's disease, dementia and  
 CC Alzheimer's disease. They are also used for drug designing and for  
 CC screening compounds that modulate the interaction of proteins of the  
 CC invention. The present sequence is human PN7740 protein  
 XX  
 XX Sequence 372 AA;  
 XX  
 Query Match 100.0%; Score 1951; DB 5; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSTAAALTLVRSGNQVRRVLLSSRLQDDRRVTPTCHSTSEPRCSRDPDGGSGSPAT 60  
 DB 1 MSTAAALTLVRSGNQVRRVLLSSRLQDDRRVTPTCHSTSEPRCSRDPDGGSGSPAT 60  
 QY 61 WDNFGIWDNRIDEPIILPPSIKYGKPIKISLENVGASQIGKKENEDRDFPAQLTDEV 120  
 DB 61 WDNFGIWDNRIDEPIILPPSIKYGKPIKISLENVGASQIGKKENEDRDFPAQLTDEV 120  
 QY 121 LYFAYVGHGGAADFCHTHMEKIMDLPKKNLETLTLTFLAFLEIDKAFSSHARLSAD 180  
 DB 121 LYFAYVGHGGAADFCHTHMEKIMDLPKKNLETLTLTFLAFLEIDKAFSSHARLSAD 180  
 QY 181 ATLLTSGTTATVALLRGIELVAVSGDSRAILCRGKPKMLTIDHTPERKDEKERIKKC 240  
 DB 181 ATLLTSGTTATVALLRGIELVAVSGDSRAILCRGKPKMLTIDHTPERKDEKERIKKC 240  
 QY 241 GGFVAVNSLGOPHVNGRLAMTRISIGDLLTKTSVGIAEPETKRIKLHADDSPFLVLTDDGI 300  
 DB 241 GGFVAVNSLGOPHVNGRLAMTRISIGDLLTKTSVGIAEPETKRIKLHADDSPFLVLTDDGI 300  
 QY 301 NFVNSQEIICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360  
 DB 301 NFVNSQEIICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360  
 QY 361 FSRSFASSGRWA 372  
 DB 361 FSRSFASSGRWA 372  
 RESULT 10  
 AAE14451  
 ID AAE14451 standard; protein; 372 AA.  
 XX  
 AC AAE14451;  
 XX  
 XX 26-MAR-2002 (first entry)  
 DT  
 XX Human protein phosphatase-1.  
 XX  
 DE Human; protein phosphatase; pp-1; immune system disorder; AIDS; allergy;  
 KW neurological disorder; developmental disorder; Alzheimer's disease;

KW cell proliferative disorder; Huntington's disease; arteriosclerosis;  
 KW renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma;  
 KW leukaemia; transgenic animal; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 104.339  
 FT Region /note= "Protein phosphatase 2C (Pp2C)"  
 FT Domain 122.130  
 FT /label= Protein\_phosphatase\_2C\_motif  
 XX  
 PN W0200196546-A2.  
 XX  
 XX 20-DEC-2001.  
 PD  
 XX  
 XX 14-JUN-2001; 2001WO-US019442.  
 PF  
 XX 16-JUN-2000; 2000US-0212447P.  
 PR 22-JUN-2000; 2000US-0213746P.  
 PR 29-JUN-2000; 2000US-0215210P.  
 PR 06-JUL-2000; 2000US-0216529P.  
 PR 13-JUL-2000; 2000US-0218080P.  
 PR 21-JUL-2000; 2000US-0220117P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX  
 XX Au-Young J, Baughn MR, Ding L, Elliott VS, Gandhi AR, Griffin JA;  
 PI Hafalia A, Kearney L, Lee EA, Lu Y, Nguyen DB, Patterson C;  
 PI Ramkumar J, Reddy R, Sanjanwala MS, Stewart EA, Tang YI, Thornton M;  
 PI Tribouley CM, Walia NK, Yang J, Yao MG, Yue H;  
 XX  
 DR WPI; 2002-090206/12.  
 DR N-PSDB; AAD24019.  
 XX  
 XX Novel polypeptide, useful for diagnosing, treating or preventing  
 PT disorders of growth and development, immune system, neurological and cell  
 PT proliferation diseases, comprises cancer protein phosphatase  
 PT polypeptides.  
 XX  
 PS Claim 1; Page 102-103; 116pp; English.  
 XX  
 XX The present sequence is human protein phosphatase (PP)-1. PP  
 CC polynucleotide and polypeptide are useful in the diagnosis, treatment and  
 CC prevention of immune system disorders, neurological disorders,  
 CC developmental disorders and cell proliferative disorders. Examples of  
 CC immune system disorders include acquired immune deficiency syndrome  
 CC (AIDS), severe combined immunodeficiency disease (SCID), adult  
 CC respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma,  
 CC atherosclerosis, Crohn's disease, atopic dermatitis, diabetes mellitus,  
 CC emphysema, Goodpasture's syndrome, gout, Graves' disease, multiple  
 CC sclerosis, myasthenia gravis, myocardial or pericardial inflammation,  
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,  
 CC rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic  
 CC sclerosis, trauma; neurological disorders include Alzheimer's disease,  
 CC Huntington's disease, dementia, epilepsy, Parkinson's disease, mental  
 CC retardation and other developmental disorders of central nervous system  
 CC such as Down's syndrome, cerebral palsy, periodic paralysis, mental  
 CC disorders including mood, anxiety, and schizophrenic disorders, seasonal  
 CC affective disorder such as akathisia, amnesia, catatonia, dyskinesia;  
 CC developmental disorders include e.g. renal tubular acidosis, Duchenne and  
 CC Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell  
 CC proliferative disorders include e.g. actinic keratosis, arteriosclerosis,  
 CC atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis and cancer  
 CC including adenocarcinoma, leukaemia. The polypeptide and polynucleotide  
 CC are further useful for analysing proteome of a tissue or a cell type, for  
 CC screening an agonist/antagonist, a compound that specifically binds to it  
 CC or its modulator. The polynucleotide is useful for creating knockin  
 CC humanised animals (pigs) or transgenic animals (mice or rats) to model  
 CC human disease, for generating a transcript image of a tissue or cell  
 CC type, which represents the global pattern of gene expression by a  
 CC particular tissue or cell type

SQ	Sequence 372 AA;	
Query Match	100.0%; Score 1951; DB 5; Length 372;	
Best Local Similarity	100.0%; Pred. No. 2.8e-206;	
Matches 372; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60	
DB	1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60	
QY	61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120	
DB	61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120	
QY	121 LYFAVVDGHHGGAADFCHTHMEKCIIMDLLPKENLETLLTFLAFLEIDKAFSSHARLSAD 180	
DB	121 LYFAVVDGHHGGAADFCHTHMEKCIIMDLLPKENLETLLTFLAFLEIDKAFSSHARLSAD 180	
QY	181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240	
DB	181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240	
QY	241 GGFVAMNSLQGPVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHHAADSFLVLTTDGI 300	
DB	241 GGFVAMNSLQGPVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHHAADSFLVLTTDGI 300	
QY	301 NFWNSQEIICDFVNOCHDPNEAAHVAHQIAQVGTEDNSTAVVVPFGAMGKYKNSINF 360	
DB	301 NFWNSQEIICDFVNOCHDPNEAAHVAHQIAQVGTEDNSTAVVVPFGAMGKYKNSINF 360	
QY	361 FRSFASGRWA 372	
DB	361 FRSFASGRWA 372	
RESULT 11		
ABU10309		
ID	ABU10309 standard; protein; 372 AA.	
AC	ABU10309;	
XX		
DT	07-AUG-2003 (first entry)	
XX		
DE	Human protein phosphatase SGP037.	
KW	Human; protein phosphatase; SGP037; cancer; blood; haematopoietic;	
KW	breast; colon; lung; prostate; cervical; brain; ovarian; bladder; kidney;	
KW	immune-related disease; cardiovascular disease; migraine;	
KW	neural-associated disease; nervous system disease; pain; rhinitis;	
KW	sexual dysfunction; mood disorder; attention disorder; hypotension;	
KW	cognition disorder; hypertension; psychotic disorder; dyskinesia;	
KW	neurological disorder; metabolic disorder; inflammatory disorder;	
KW	rheumatoid arthritis; chronic inflammatory bowel disease; asthma;	
KW	chronic inflammatory pelvic disease; multiple sclerosis; psoriasis;	
KW	osteoarthritis; psoriasis; atherosclerosis; autoimmune; neoplastic;	
KW	organ transplant rejection; cytostatic; neuroprotective; analgesic;	
KW	hypotensive; anticonvulsant; antiarthritic; antirheumatic;	
KW	antiinflammatory; antiasthmatic; osteopathic; antipsoriatic;	
KW	antiarteriosclerotic; immunosuppressive; enzyme.	
OS	Homo sapiens.	
XX		
FN	US2003027308-A1.	
PD	06-FEB-2003.	
XX		
PE	13-NOV-2001; 2001US-00986992.	
XX		
PR	30-MAY-2000; 2000US-0208291P.	
PR	13-NOV-2000; 2000US-0246974P.	
XX		
PA	(SUGS-) SUGEN INC.	
XX		
PI	Plowman GD, Whyte D, Manning G;	
XX		
DR	WPI; 2003-466146/44.	
DR	N-PSDB; ABX95873.	
XX		
PT	New isolated, enriched or purified nucleic acid molecule encoding a	
PT	phosphatase polypeptide, useful for treating diseases, e.g. cancers, or	
PT	immune-related cardiovascular, brain and neuronal, metabolic or	
PT	inflammatory disorders.	
XX		
PS	Claim 1; Fig 2; 45pp; English.	
XX		
CC	The present invention relates to the isolation of a novel human protein	
CC	phosphatase designated SGP037, and the polynucleotide sequence encoding	
CC	it. The gene encoding human SGP037 maps to chromosome 4q21. The SGP037	
CC	polypeptide and the polynucleotide sequence encoding it are useful for	
CC	treating diseases or disorders such as cancers (e.g. cancer of the blood	
CC	or haematopoietic origin, breast, colon, lung, prostate, cervical, brain,	
CC	ovarian, bladder or kidney), immune-related diseases and disorders,	
CC	cardiovascular diseases, brain and neuronal-associated diseases (e.g.	
CC	central or peripheral nervous system diseases, migraines, pain, sexual	
CC	dysfunction, mood disorders, attention disorders, cognition disorders,	
CC	hypotension, hypertension, psychotic disorders, neurological disorders or	
CC	dyskinesias), metabolic disorders, and inflammatory disorders (e.g.	
CC	rheumatoid arthritis, chronic inflammatory bowel disease, chronic	
CC	inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,	
CC	psoriasis, atherosclerosis, rhinitis, autoimmunity or organ transplant	
CC	rejection). The present sequence represents human SGP037	
XX		
SQ	Sequence 372 AA;	
Query Match	100.0%; Score 1951; DB 6; Length 372;	
Best Local Similarity	100.0%; Pred. No. 2.8e-206;	
Matches 372; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60	
DB	1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60	
QY	61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120	
DB	61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120	
QY	121 LYFAVVDGHHGGAADFCHTHMEKCIIMDLLPKENLETLLTFLAFLEIDKAFSSHARLSAD 180	
DB	121 LYFAVVDGHHGGAADFCHTHMEKCIIMDLLPKENLETLLTFLAFLEIDKAFSSHARLSAD 180	
QY	181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240	
DB	181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240	
QY	241 GGFVAMNSLQGPVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHHAADSFLVLTTDGI 300	
DB	241 GGFVAMNSLQGPVNGRLAMTRISIGDLDLKTSIGVIAEPETKRIKLHHAADSFLVLTTDGI 300	
QY	301 NFWNSQEIICDFVNOCHDPNEAAHVAHQIAQVGTEDNSTAVVVPFGAMGKYKNSINF 360	
DB	301 NFWNSQEIICDFVNOCHDPNEAAHVAHQIAQVGTEDNSTAVVVPFGAMGKYKNSINF 360	
QY	361 FRSFASGRWA 372	
DB	361 FRSFASGRWA 372	
RESULT 12		
AAO23055		
ID	AAO23055 standard; protein; 372 AA.	
XX		
AC	AAO23055;	
XX		
DT	17-SEP-2003 (first entry)	
XX		
DE	Human serine/threonine PP2C phosphatase SGP037 protein.	

XX Cytostatic; immunosuppressive; cardiovascular; hypotensive; hypertensive;  
 KW antiemetic; analgesic; nootropic; tranquilizer; antirheumatic; brain;  
 KW antiarthritic; antiinflammatory; gynaecological; neuroprotective; ocular;  
 KW antiasthmatic; osteopathic; antipsoriatic; antiarteriosclerotic; obesity;  
 KW antiallergic; serine threonine phosphatase; STP; PP2C; cancer; immune;  
 KW cardiovascular disease; neuronal; sexual dysfunction; migraine; glaucoma;  
 KW psychotic; neurological; schizophrenia; metabolic; inflammatory; SGP037;  
 KW multiple sclerosis; viral infection; HIV; transgenic; gene therapy;  
 KW enzyme; human; chromosome 4q21.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Region 104..339  
 FT /note= "Catalytic region"  
 XX  
 PN WO2003042390-A1.  
 XX  
 XX 22-MAY-2003.  
 XX  
 PF 13-NOV-2001; 2001WO-US043063.  
 XX  
 PR 13-NOV-2001; 2001WO-US043063.  
 XX  
 XX (FLOW/) FLOWMAN G D.  
 XX  
 XX Plowman GD, Manning G, Whyte D;  
 XX  
 DR WPI; 2003-449576/42.  
 DR N-PSDB; AAL55773.  
 XX  
 XX New phosphatase nucleic acid molecule and polypeptide, useful for  
 PT diagnosing or treating phosphatase-related disorders such as cancers,  
 PT immune-related disorders, cardiovascular disease, and inflammatory  
 PT disorders.  
 XX  
 XX Claim 26; Fig 2; 152pp; English.  
 PS  
 XX  
 CC The invention relates to a novel isolated nucleic acid molecule encoding  
 CC a serine/threonine phosphatase (STP) polypeptide which is a member of the  
 CC PP2C family. PP2C phosphatases are involved in a number of cellular  
 CC processes including modulation of integrin signal transduction and  
 CC regulation of the TAK1 signalling pathway, cellular channels, cyclin  
 CC dependent kinases and the Ras pathway. The methods and compositions of  
 CC the present invention may be useful during the diagnosis or treatment of  
 CC a variety of disorders including cancers, immune-related and  
 CC cardiovascular disease, brain or neuronal-associated diseases such as  
 CC sexual dysfunction and migraine, psychotic and neurological disorders  
 CC e.g. schizophrenia and metabolic disorders such as obesity. Furthermore,  
 CC ocular disease, such as glaucoma and inflammatory disorders e.g. multiple  
 CC sclerosis may be addressed, as well as viral infections caused by HIV and  
 CC other pathological agents. Finally, the molecules of the invention may be  
 CC utilised in the production of transgenic animals and during gene therapy.  
 CC The current sequence is that of the human serine/threonine PP2C  
 CC phosphatase SGP037 protein of the invention  
 XX  
 XX Sequence 372 AA;  
 SQ  
 Query Match 100.0%; Score 1951; DB 6; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSTAALITLVRSQGNQVRRVLLSSRLIQDDRVTPTCHSSTSPRCRFPDGGSGPAT 60  
 DB 1 MSTAALITLVRSQGNQVRRVLLSSRLIQDDRVTPTCHSSTSPRCRFPDGGSGPAT 60  
 QY 61 WDNFGIWDNRIDEPIILPPSIKYCKPIKISLENVGCSAQIGKKEKEDREDFQAQLTDEV 120  
 DB 61 WDNFGIWDNRIDEPIILPPSIKYCKPIKISLENVGCSAQIGKKEKEDREDFQAQLTDEV 120  
 QY 121 LYFAVYDGHGGAADFCHTHMEKCIIMDLLPEKKNLETLTLTFLAFLDKAFSSHARLSAD 180

DB 121 LYFAVYDGHGGAADFCHTHMEKCIIMDLLPEKKNLETLTLTFLAFLDKAFSSHARLSAD 180  
 QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDKERIKKC 240  
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPMKLTIDHTPERKDKERIKKC 240  
 QY 241 GGFVAVNSLGQPHVNGRLAMWTRISIGDLDKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300  
 DB 241 GGFVAVNSLGQPHVNGRLAMWTRISIGDLDKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300  
 QY 301 NFMVNSQIEICDFVNOCHDNEAAHVAITEQAIQYGTEDNSTAVVVPFGAMGKYKNSEINFS 360  
 DB 301 NFMVNSQIEICDFVNOCHDNEAAHVAITEQAIQYGTEDNSTAVVVPFGAMGKYKNSEINFS 360  
 QY 361 FRSFPASSGRWA 372  
 DB 361 FRSFPASSGRWA 372  
 RESULT 13  
 ADB66824  
 ID ADB66824 standard; protein; 372 AA.  
 XX  
 AC ADB66824;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 XX Human PN7740.  
 XX  
 KW human; drug candidate screening; neurodegenerative disorder;  
 KW Huntington's disease; Parkinson's disease; dementia; Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002115119-A1.  
 XX  
 PD 22-AUG-2002.  
 XX  
 PF 10-OCT-2001; 2001US-00973063.  
 XX  
 PR 17-OCT-2000; 2000US-0240790P.  
 XX  
 XX (MYRI-) MYRIAD GENETICS INC.  
 XX  
 PI Roch J, Bartel PL, Heichman K;  
 XX  
 DR WPI; 2003-719962/68.  
 DR N-PSDB; ADB66827.  
 XX  
 XX Screening drug candidates for modulating interaction of complexes of  
 PT protein, by combining protein in the presence or absence of a drug to  
 PT form first and second complex, and measuring and comparing both the  
 PT complexes.  
 XX  
 XX Example 2; Page 22; 36pp; English.  
 XX  
 CC The invention relates to a method of screening drug candidates for  
 CC modulating interaction of proteins in a complex. The method is useful for  
 CC screening drug candidates useful in treating neurodegenerative disorder,  
 CC by measuring the activity of a protein selected from Mint2 and PDE-9A in  
 CC the presence or absence of the drug, and comparing the activity measured,  
 CC where if there is a difference in activity, then the drug is a drug  
 CC candidate for treating the neurodegenerative disorder. The  
 CC neurodegenerative disorder is Huntington's disease, Parkinson's disease,  
 CC dementia, or Alzheimer's disease, preferably Alzheimer's disease. The  
 CC drug, modulator or compound identified by the methods of the invention  
 CC are useful for treating a neurodegenerative disorder. The present  
 CC sequence represents the amino acid sequence of human PN7740.  
 XX  
 XX Sequence 372 AA;  
 SQ  
 Query Match 100.0%; Score 1951; DB 7; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60  
 DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60  
 QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLVNVCASQIGRKENEDRFPDFAQLTDEV 120  
 DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLVNVCASQIGRKENEDRFPDFAQLTDEV 120  
 QY 121 LYFVAVDGHGGGAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180  
 DB 121 LYFVAVDGHGGGAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180  
 QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMKLTIDHTPERKDEKERIKK 240  
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMKLTIDHTPERKDEKERIKK 240  
 QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300  
 DB 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300  
 QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGAMGKYKNSINF 360  
 DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGAMGKYKNSINF 360  
 QY 361 FSRSPASSGRWA 372  
 DB 361 FSRSPASSGRWA 372

RESULT 14  
 ADD73452  
 ID ADD73452 standard; protein; 372 AA.  
 XX  
 AC ADD73452;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Novel human protein PN7740.  
 XX  
 KW nontropic; neuroprotective; antiparkinsonian; protein binding modulator;  
 KW drug screening; neurodegenerative disorder; Huntington's Disease;  
 KW Parkinson's Disease; dementia; Alzheimer's Disease; AD; APP; presenilin;  
 KW protein-protein interaction; drug target identification; human;  
 KW yeast two-hybrid assay; PN7740.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003186317-A1.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PF 09-OCT-2001; 2001US-00971782.  
 XX  
 PR 17-OCT-2000; 2000US-0240790P.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.  
 XX  
 PI Roch J, Bartel PL, Heichman K;  
 XX  
 DR WPI; 2003-852417/79.  
 DR N-PSDB; ADD73455.  
 XX  
 PT In vitro screening for drug useful for treating neurodegenerative  
 PT disorder, e.g. Alzheimer's Disease, involves comparing the amount of two  
 PT complexes formed from combined proteins of protein complex in the  
 PT presence and absence of drug.  
 XX  
 PS Example 2-33; SEQ ID NO 4; 36pp; English.  
 XX  
 CC The invention describes screening a drug in vitro by combining proteins  
 CC of a protein complex in the presence of a drug to form a first complex;

CC combining the proteins in the absence of the drug to form a second  
 CC complex, measuring the amount of the two complexes; and comparing the  
 CC amount of the first complex with the amount of the second complex. The  
 CC method is useful for screening drug candidates capable of modulating a  
 CC interaction of the proteins of a protein complex, useful for treating a  
 CC neurodegenerative disorder, e.g. Huntington's Disease, Parkinson's  
 CC Disease, dementia or Alzheimer's Disease (AD). The inventive method  
 CC provides for the discovery of additional proteins interacting with  
 CC various domains of the major Alzheimer proteins, including APP and the  
 CC presenilins. It can also identify the protein-protein interactions that  
 CC are involved in Alzheimer's Disease (AD) pathogenesis, and to identify  
 CC drug targets. This is the amino acid sequence of a novel human protein  
 CC PN7740 identified using yeast two-hybrid assay with a human brain bait  
 CC protein.  
 XX  
 SQ Sequence 372 AA;  
 Query Match 100.0%; Score 1951; DB 7; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-206;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60  
 DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDPGSGSPAT 60  
 QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLVNVCASQIGRKENEDRFPDFAQLTDEV 120  
 DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLVNVCASQIGRKENEDRFPDFAQLTDEV 120  
 QY 121 LYFVAVDGHGGGAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180  
 DB 121 LYFVAVDGHGGGAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLEIDKAFSSHARLSAD 180  
 QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMKLTIDHTPERKDEKERIKK 240  
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRGKPKMKLTIDHTPERKDEKERIKK 240  
 QY 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300  
 DB 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300  
 QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGAMGKYKNSINF 360  
 DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAIYGTEDNSTAVVVPFGAMGKYKNSINF 360  
 QY 361 FSRSPASSGRWA 372  
 DB 361 FSRSPASSGRWA 372

RESULT 15  
 ADQ14718  
 ID ADQ14718 standard; protein; 372 AA.  
 XX  
 AC ADQ14718;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Human protein phosphatase SGP037.  
 XX  
 KW Human; enzyme; protein phosphatase; SGP037; chromosome 4q21;  
 KW acute lymphoblastic leukaemia; cancer; immune-related disease;  
 KW cardiovascular disease; brain disease; neuronal-associated disease;  
 KW metabolic disorder; inflammatory disorder; rheumatoid arthritis;  
 KW chronic inflammatory bowel disease; chronic inflammatory pelvis disease;  
 KW multiple sclerosis; asthma; osteoarthritis; psoriasis; atherosclerosis;  
 KW rhinitis; autoimmunity; organ transplant rejection;  
 KW central nervous system disease; migraine; pain; sexual dysfunction;  
 KW mood disorder; attention disorder; cognition disorder; hypotension;  
 KW hypertension; psychotic disorder; neurological disorder; dyskinesia.  
 OS Homo sapiens.  
 XX



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